



Sequence Listing

<110> Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan l.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.

<120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same

<130> P2830P1C7

<140> 10/006130
<141> 2001-12-06

<150> 60/098716
<151> 1998-09-01

<150> 60/098723
<151> 1998-09-01

<150> 60/098749
<151> 1998-09-01

<150> 60/098750
<151> 1998-09-01

<150> 60/098803
<151> 1998-09-02

<150> 60/098821
<151> 1998-09-02

<150> 60/098843
<151> 1998-09-02

<150> 60/099536
<151> 1998-09-09

<150> 60/099596
<151> 1998-09-09

<150> 60/099598
<151> 1998-09-09

<150> 60/099602
<151> 1998-09-09

<150> 60/099642
<151> 1998-09-09

<150> 60/099741
<151> 1998-09-10

<150> 60/099754
<151> 1998-09-10

<150> 60/099763
<151> 1998-09-10

<150> 60/099792
<151> 1998-09-10

<150> 60/099808
<151> 1998-09-10

<150> 60/099812
<151> 1998-09-10

<150> 60/099815
<151> 1998-09-10

<150> 60/099816
<151> 1998-09-10

<150> 60/100385
<151> 1998-09-15

<150> 60/100388
<151> 1998-09-15

<150> 60/100390
<151> 1998-09-15

<150> 60/100584
<151> 1998-09-16

<150> 60/100627
<151> 1998-09-16

<150> 60/100661
<151> 1998-09-16

<150> 60/100662
<151> 1998-09-16

<150> 60/100664
<151> 1998-09-16

<150> 60/100683
<151> 1998-09-17

<150> 60/100684
<151> 1998-09-17

<150> 60/100710
<151> 1998-09-17

<150> 60/100711
<151> 1998-09-17

<150> 60/100848
<151> 1998-09-18

<150> 60/100849
<151> 1998-09-18

<150> 60/100919
<151> 1998-09-17

<150> 60/100930
<151> 1998-09-17

<150> 60/101014
<151> 1998-09-18

<150> 60/101068
<151> 1998-09-18

<150> 60/101071
<151> 1998-09-18

<150> 60/101279
<151> 1998-09-22

<150> 60/101471
<151> 1998-09-23

<150> 60/101472
<151> 1998-09-23

<150> 60/101474
<151> 1998-09-23

<150> 60/101475
<151> 1998-09-23

<150> 60/101476
<151> 1998-09-23

<150> 60/101477
<151> 1998-09-23

<150> 60/101479
<151> 1998-09-23

<150> 60/101738
<151> 1998-09-24

<150> 60/101741
<151> 1998-09-24

<150> 60/101743
<151> 1998-09-24

<150> 60/101915
<151> 1998-09-24

<150> 60/101916
<151> 1998-09-24

<150> 60/102207
<151> 1998-09-29

<150> 60/102240
<151> 1998-09-29

<150> 60/102307
<151> 1998-09-29

<150> 60/102330
<151> 1998-09-29

<150> 60/102331
<151> 1998-09-29

<150> 60/102484
<151> 1998-09-30

<150> 60/102487
<151> 1998-09-30

<150> 60/102570
<151> 1998-09-30

<150> 60/102571
<151> 1998-09-30

<150> 60/102684
<151> 1998-10-01

<150> 60/102687
<151> 1998-10-01

<150> 60/102965
<151> 1998-10-02

<150> 60/103258
<151> 1998-10-06

<150> 60/103314
<151> 1998-10-07

<150> 60/103315
<151> 1998-10-07

<150> 60/103328
<151> 1998-10-07

<150> 60/103395
<151> 1998-10-07

<150> 60/103396
<151> 1998-10-07

<150> 60/103401
<151> 1998-10-07

<150> 60/103449
<151> 1998-10-06

<150> 60/103633
<151> 1998-10-08

<150> 60/103678
<151> 1998-10-08

<150> 60/103679
<151> 1998-10-08

<150> 60/103711
<151> 1998-10-08

<150> 60/104257
<151> 1998-10-14

<150> 60/104987
<151> 1998-10-20

<150> 60/105000
<151> 1998-10-20

<150> 60/105002
<151> 1998-10-20

<150> 60/105104
<151> 1998-10-21

<150> 60/105169
<151> 1998-10-22

<150> 60/105266
<151> 1998-10-22

<150> 60/105693
<151> 1998-10-26

<150> 60/105694
<151> 1998-10-26

<150> 60/105807
<151> 1998-10-27

<150> 60/105881
<151> 1998-10-27

<150> 60/105882
<151> 1998-10-27

<150> 60/106023
<151> 1998-10-28

<150> 60/106029
<151> 1998-10-28

<150> 60/106030
<151> 1998-10-28

<150> 60/106032
<151> 1998-10-28

<150> 60/106033
<151> 1998-10-28

<150> 60/106062
<151> 1998-10-27

<150> 60/106178
<151> 1998-10-28

<150> 60/106248
<151> 1998-10-29

<150> 60/106384
<151> 1998-10-29

<150> 60/108500
<151> 1998-10-29

<150> 60/106464
<151> 1998-10-30

<150> 60/106856
<151> 1998-11-03

<150> 60/106902
<151> 1998-11-03

<150> 60/106905
<151> 1998-11-03

<150> 60/106919
<151> 1998-11-03

<150> 60/106932
<151> 1998-11-03

<150> 60/106934
<151> 1998-11-03

<150> 60/107783
<151> 1998-11-10

<150> 60/108775
<151> 1998-11-17

<150> 60/108779
<151> 1998-11-17

<150> 60/108787
<151> 1998-11-17

<150> 60/108788
<151> 1998-11-17

<150> 60/108801
<151> 1998-11-17

<150> 60/108802
<151> 1998-11-17

<150> 60/108806
<151> 1998-11-17

<150> 60/108807
<151> 1998-11-17

<150> 60/108848
<151> 1998-11-18

<150> 60/108849
<151> 1998-11-18

<150> 60/108850
<151> 1998-11-18

<150> 60/108851
<151> 1998-11-18

<150> 60/108852
<151> 1998-11-18

<150> 60/108858
<151> 1998-11-18

<150> 60/108867
<151> 1998-11-17

<150> 60/108904
<151> 1998-11-18

<150> 60/108925
<151> 1998-11-17

<150> 60/113296
<151> 1998-12-22

<150> 60/114223
<151> 1998-12-30

<150> 60/129674
<151> 1999-04-16

<150> 60/141037
<151> 1999-06-23

<150> 60/144758
<151> 1999-07-20

<150> 60/145698
<151> 1999-07-26

<150> 60/162506
<151> 1999-10-29

<150> 09/218517
<151> 1998-12-22

<150> 09/284291
<151> 1999-04-12

<150> 09/403297
<151> 1999-10-18

<150> 09/872035
<151> 2001-06-01

<150> 09/882636
<151> 2001-06-14

<150> 09/946374
<151> 2001-09-04

<150> PCT/US99/00106
<151> 1999-01-05

<150> PCT/US99/20111
<151> 1999-09-01

<150> PCT/US99/21194
<151> 1999-09-15

<150> PCT/US99/28313
<151> 1999-11-30

<150> PCT/US99/28551
<151> 1999-12-02

<150> PCT/US99/30095
<151> 1999-12-16

<150> PCT/US00/00219
<151> 2000-01-05

<150> PCT/US00/00376
<151> 2000-01-06

<150> PCT/US00/03565
<151> 2000-02-11

<150> PCT/US00/04342
<151> 2000-02-18

<150> PCT/US00/05004
<151> 2000-02-24

<150> PCT/US00/05841
<151> 2000-03-02

<150> PCT/US00/06884
<151> 2000-03-15

<150> PCT/US00/13705
<151> 2000-05-17

<150> PCT/US00/14042
<151> 2000-05-22

<150> PCT/US00/14941
<151> 2000-05-30

<150> PCT/US00/15264
<151> 2000-06-02

<150> PCT/US00/23328
<151> 2000-08-24

<150> PCT/US00/23522
<151> 2000-08-23

<150> PCT/US00/30873
<151> 2000-11-10

<150> PCT/US00/30952
<151> 2000-11-08

<150> PCT/US00/32678
<151> 2000-12-01

<150> PCT/US01/06520
<151> 2001-02-28

<150> PCT/US01/06666
<151> 2001-03-01

<150> PCT/US01/17800
<151> 2001-06-01

<150> PCT/US01/19692
<151> 2001-06-20

<150> PCT/US01/21066
<151> 2001-06-29

<150> PCT/US01/21735

<151> 2001-07-09

<160> 477

<210> 1

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 1

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 2

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 2

caggaaacag ctatgaccac ctgcacacct gcaaataccat t 41

<210> 3

<211> 1110

<212> DNA

<213> Homo sapiens

<400> 3

ccaatcgccc ggtgcggtgg tgcagggctct cgggctagtc atggcggtccc 50
cgtctcggag actgcagact aaaccagtca ttacttgttt caagagcgtt 100
ctgctaattct acacttttat tttctggatc actggcggtta tccttcttgc 150
agttggcatt tggggcaagg tgagcctgga gaattacttt tctcttttaa 200
atgagaaggc caccaatgtc cccttcgtgc tcattgctac tggtaaccgtc 250
attattcttt tgggcacctt tggttgtttt gctacctgcc gagcttctgc 300
atggatgcta aaactgtatg caatgtttct gactctcgtt tttttggtcg 350
aactgggtcgc tgccatcgta ggatttgttt tcagacatga gattaagaac 400
agctttaaga ataattatga gaaggctttg aagcagtata actctacagg 450
agattataga agccatgcag tagacaagat ccaaaatacg ttgcattggt 500
gtggtgtcac cgattataga gattggacag atactaatta ttactcagaa 550
aaaggatttc ctaagagttg ctgtaaactt gaagattgta ctccacagag 600

agatgcagac aaagtaaaca atgaaggttg ttttataaag gtgatgacca 650
 ttatagagtc agaaatggga gtcgttgacag gaatttcctt tggagttgct 700
 tgcttccaac tgattggaat ctttctcgcc tactgccwct ctcgtgccat 750
 aacaaataac cagtatgaga tagtgtaacc caatgtatct gtgggcctat 800
 tcctctctac ctttaaggac atttagggtc cccctgtga attagaaagt 850
 tgcttggtg gagaaactgac aacactactt actgatagac caaaaaacta 900
 caccagtagg ttgattcaat caagatgtat gtagacctaa aactacacca 950
 ataggctgat tcaatcaaga tccgtgctcg cagtgggctg attcaatcaa 1000
 gatgtatgtt tgctatgttc taagtccacc ttctatccca ttcattgtag 1050
 atcgttgaaa ccctgtatcc ctctgaaaca ctggaagagc tagtaaattg 1100
 taaatgaagt 1110

<210> 4
 <211> 245
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-42
 <223> Signal Peptide

<220>
 <221> TRANSMEM
 <222> 19-42, 61-83, 92-114, 209-230
 <223> Transmembrane Domains

<220>
 <221> misc_feature
 <222> 69-80, 211-222
 <223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

<220>
 <221> misc_feature
 <222> 75-81, 78-84, 210-216, 214-220, 226-232
 <223> N-Myristoylation Site.

<220>
 <221> misc_feature
 <222> 134-138
 <223> N-Glycosylation Site.

<220>
 <221> misc_feature
 <222> 160-168, 160-169
 <223> Tyrosine Kinase Phosphorylation Site.

<223> unknown amino acid

```

400> 4
Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr
      1          5          10          15

```

Cys Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile
20 25 30

Thr Gly Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser
35 40 45

Leu Glu Asn Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val
50 55 60

Pro Phe Val Leu Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly
65 75

Thr Phe Gly Cys Phe Ala Thr Cys Arg Ala Ser Ala Trp Met Leu
80 85 90

Lys Leu Tyr Ala Met Phe Leu Thr Leu Val Phe Leu Val Glu Leu
95 100 105

Val Ala Ala Ile Val Gly Phe Val Phe Arg His Glu Ile Lys Asn
110 115 120

Ser Phe Lys Asn Asn Tyr Glu Lys Ala Leu Lys Gln Tyr Asn Ser
125 130 135

Thr Gly Asp Tyr Arg Ser His Ala Val Asp Lys Ile Gln Asn Thr
140 145 150

Leu His Cys Cys Gly Val Thr Asp Tyr Arg Asp Trp Thr Asp Thr
155 160 165

Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser Cys Cys Lys Leu
170 175 180

Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val Asn Asn Glu
185 190 195

Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu Met Gly
200 205 210

Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu Ile
215 220 225

Gly Ile Phe Leu Ala Tyr Cys Xaa Ser Arg Ala Ile Thr Asn Asn
230 235 240

Gln Tyr Glu Ile Val
245



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/006,130

DATE: 12/17/2001
TIME: 11:12:13

Input Set : A:\Seq_List_for_P2830P1C7.wpd
Output Set: N:\CRF3\12172001\J006130.raw

pb

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Baker, Kevin P.
4 Botstein, David
5 Desnoyers, Luc
6 Eaton, Dan l.
7 Ferrara, Napoleone
8 Fong, Sherman
9 Gao, Wei-Qiang
10 Goddard, Audrey
11 Godowski, Paul J.
12 Grimaldi, Christopher J.
13 Gurney, Austin L.
14 Hillan, Kenneth J.
15 Pan, James
16 Paoni, Nicholas F.
18 <120> TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
19 Acids Encoding the Same
21 <130> FILE REFERENCE: P2830P1C7
C--> 23 <140> CURRENT APPLICATION NUMBER: US/10/006,130
C--> 23 <141> CURRENT FILING DATE: 2001-12-06
23 <150> PRIOR APPLICATION NUMBER: 60/098716
24 <151> PRIOR FILING DATE: 1998-09-01
26 <150> PRIOR APPLICATION NUMBER: 60/098723
27 <151> PRIOR FILING DATE: 1998-09-01
29 <150> PRIOR APPLICATION NUMBER: 60/098749
30 <151> PRIOR FILING DATE: 1998-09-01
32 <150> PRIOR APPLICATION NUMBER: 60/098750
33 <151> PRIOR FILING DATE: 1998-09-01
35 <150> PRIOR APPLICATION NUMBER: 60/098803
36 <151> PRIOR FILING DATE: 1998-09-02
38 <150> PRIOR APPLICATION NUMBER: 60/098821
39 <151> PRIOR FILING DATE: 1998-09-02
41 <150> PRIOR APPLICATION NUMBER: 60/098843
42 <151> PRIOR FILING DATE: 1998-09-02
44 <150> PRIOR APPLICATION NUMBER: 60/099536
45 <151> PRIOR FILING DATE: 1998-09-09
47 <150> PRIOR APPLICATION NUMBER: 60/099596
48 <151> PRIOR FILING DATE: 1998-09-09
50 <150> PRIOR APPLICATION NUMBER: 60/099598
51 <151> PRIOR FILING DATE: 1998-09-09
53 <150> PRIOR APPLICATION NUMBER: 60/099602
54 <151> PRIOR FILING DATE: 1998-09-09
56 <150> PRIOR APPLICATION NUMBER: 60/099642
57 <151> PRIOR FILING DATE: 1998-09-09
59 <150> PRIOR APPLICATION NUMBER: 60/099741
60 <151> PRIOR FILING DATE: 1998-09-10
62 <150> PRIOR APPLICATION NUMBER: 60/099754
63 <151> PRIOR FILING DATE: 1998-09-10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/006,130

DATE: 12/17/2001

TIME: 11:12:13

Input Set : A:\Seq_List_for_P2830PlC7.wpd
Output Set: N:\CRF3\12172001\J006130.raw

65 <150> PRIOR APPLICATION NUMBER: 60/099763
66 <151> PRIOR FILING DATE: 1998-09-10
68 <150> PRIOR APPLICATION NUMBER: 60/099792
69 <151> PRIOR FILING DATE: 1998-09-10
71 <150> PRIOR APPLICATION NUMBER: 60/099808
72 <151> PRIOR FILING DATE: 1998-09-10
74 <150> PRIOR APPLICATION NUMBER: 60/099812
75 <151> PRIOR FILING DATE: 1998-09-10
77 <150> PRIOR APPLICATION NUMBER: 60/099815
78 <151> PRIOR FILING DATE: 1998-09-10
80 <150> PRIOR APPLICATION NUMBER: 60/099816
81 <151> PRIOR FILING DATE: 1998-09-10
83 <150> PRIOR APPLICATION NUMBER: 60/100385
84 <151> PRIOR FILING DATE: 1998-09-15
86 <150> PRIOR APPLICATION NUMBER: 60/100388
87 <151> PRIOR FILING DATE: 1998-09-15
89 <150> PRIOR APPLICATION NUMBER: 60/100390
90 <151> PRIOR FILING DATE: 1998-09-15
92 <150> PRIOR APPLICATION NUMBER: 60/100584
93 <151> PRIOR FILING DATE: 1998-09-16
95 <150> PRIOR APPLICATION NUMBER: 60/100627
96 <151> PRIOR FILING DATE: 1998-09-16
98 <150> PRIOR APPLICATION NUMBER: 60/100661
99 <151> PRIOR FILING DATE: 1998-09-16
101 <150> PRIOR APPLICATION NUMBER: 60/100662
102 <151> PRIOR FILING DATE: 1998-09-16
104 <150> PRIOR APPLICATION NUMBER: 60/100664
105 <151> PRIOR FILING DATE: 1998-09-16
107 <150> PRIOR APPLICATION NUMBER: 60/100683
108 <151> PRIOR FILING DATE: 1998-09-17
110 <150> PRIOR APPLICATION NUMBER: 60/100684
111 <151> PRIOR FILING DATE: 1998-09-17
113 <150> PRIOR APPLICATION NUMBER: 60/100710
114 <151> PRIOR FILING DATE: 1998-09-17
116 <150> PRIOR APPLICATION NUMBER: 60/100711
117 <151> PRIOR FILING DATE: 1998-09-17
119 <150> PRIOR APPLICATION NUMBER: 60/100848
120 <151> PRIOR FILING DATE: 1998-09-18
122 <150> PRIOR APPLICATION NUMBER: 60/100849
123 <151> PRIOR FILING DATE: 1998-09-18
125 <150> PRIOR APPLICATION NUMBER: 60/100919
126 <151> PRIOR FILING DATE: 1998-09-17
128 <150> PRIOR APPLICATION NUMBER: 60/100930
129 <151> PRIOR FILING DATE: 1998-09-17
131 <150> PRIOR APPLICATION NUMBER: 60/101014
132 <151> PRIOR FILING DATE: 1998-09-18
134 <150> PRIOR APPLICATION NUMBER: 60/101068
135 <151> PRIOR FILING DATE: 1998-09-18
137 <150> PRIOR APPLICATION NUMBER: 60/101071

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/006,130

DATE: 12/17/2001

TIME: 11:12:13

Input Set : A:\Seq_List_for_P2830P1C7.wpd

Output Set: N:\CRF3\12172001\J006130.raw

138 <151> PRIOR FILING DATE: 1998-09-18
140 <150> PRIOR APPLICATION NUMBER: 60/101279
141 <151> PRIOR FILING DATE: 1998-09-22
143 <150> PRIOR APPLICATION NUMBER: 60/101471
144 <151> PRIOR FILING DATE: 1998-09-23
146 <150> PRIOR APPLICATION NUMBER: 60/101472
147 <151> PRIOR FILING DATE: 1998-09-23
149 <150> PRIOR APPLICATION NUMBER: 60/101474
150 <151> PRIOR FILING DATE: 1998-09-23
152 <150> PRIOR APPLICATION NUMBER: 60/101475
153 <151> PRIOR FILING DATE: 1998-09-23
155 <150> PRIOR APPLICATION NUMBER: 60/101476
156 <151> PRIOR FILING DATE: 1998-09-23
158 <150> PRIOR APPLICATION NUMBER: 60/101477
159 <151> PRIOR FILING DATE: 1998-09-23
161 <150> PRIOR APPLICATION NUMBER: 60/101479
162 <151> PRIOR FILING DATE: 1998-09-23
164 <150> PRIOR APPLICATION NUMBER: 60/101738
165 <151> PRIOR FILING DATE: 1998-09-24
167 <150> PRIOR APPLICATION NUMBER: 60/101741
168 <151> PRIOR FILING DATE: 1998-09-24
170 <150> PRIOR APPLICATION NUMBER: 60/101743
171 <151> PRIOR FILING DATE: 1998-09-24
173 <150> PRIOR APPLICATION NUMBER: 60/101915
174 <151> PRIOR FILING DATE: 1998-09-24
176 <150> PRIOR APPLICATION NUMBER: 60/101916
177 <151> PRIOR FILING DATE: 1998-09-24
179 <150> PRIOR APPLICATION NUMBER: 60/102207
180 <151> PRIOR FILING DATE: 1998-09-29
182 <150> PRIOR APPLICATION NUMBER: 60/102240
183 <151> PRIOR FILING DATE: 1998-09-29
185 <150> PRIOR APPLICATION NUMBER: 60/102307
186 <151> PRIOR FILING DATE: 1998-09-29
188 <150> PRIOR APPLICATION NUMBER: 60/102330
189 <151> PRIOR FILING DATE: 1998-09-29
191 <150> PRIOR APPLICATION NUMBER: 60/102331
192 <151> PRIOR FILING DATE: 1998-09-29
194 <150> PRIOR APPLICATION NUMBER: 60/102484
195 <151> PRIOR FILING DATE: 1998-09-30
197 <150> PRIOR APPLICATION NUMBER: 60/102487
198 <151> PRIOR FILING DATE: 1998-09-30
200 <150> PRIOR APPLICATION NUMBER: 60/102570
201 <151> PRIOR FILING DATE: 1998-09-30
203 <150> PRIOR APPLICATION NUMBER: 60/102571
204 <151> PRIOR FILING DATE: 1998-09-30
206 <150> PRIOR APPLICATION NUMBER: 60/102684
207 <151> PRIOR FILING DATE: 1998-10-01
209 <150> PRIOR APPLICATION NUMBER: 60/102687
210 <151> PRIOR FILING DATE: 1998-10-01

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/006,130

DATE: 12/17/2001

TIME: 11:12:13

Input Set : A:\Seq_List_for_P2830P1C7.wpd

Output Set: N:\CRF3\12172001\J006130.raw

212 <150> PRIOR APPLICATION NUMBER: 60/102965
213 <151> PRIOR FILING DATE: 1998-10-02
215 <150> PRIOR APPLICATION NUMBER: 60/103258
216 <151> PRIOR FILING DATE: 1998-10-06
218 <150> PRIOR APPLICATION NUMBER: 60/103314
219 <151> PRIOR FILING DATE: 1998-10-07
221 <150> PRIOR APPLICATION NUMBER: 60/103315
222 <151> PRIOR FILING DATE: 1998-10-07
224 <150> PRIOR APPLICATION NUMBER: 60/103328
225 <151> PRIOR FILING DATE: 1998-10-07
227 <150> PRIOR APPLICATION NUMBER: 60/103395
228 <151> PRIOR FILING DATE: 1998-10-07
230 <150> PRIOR APPLICATION NUMBER: 60/103396
231 <151> PRIOR FILING DATE: 1998-10-07
233 <150> PRIOR APPLICATION NUMBER: 60/103401
234 <151> PRIOR FILING DATE: 1998-10-07
236 <150> PRIOR APPLICATION NUMBER: 60/103449
237 <151> PRIOR FILING DATE: 1998-10-06
239 <150> PRIOR APPLICATION NUMBER: 60/103633
240 <151> PRIOR FILING DATE: 1998-10-08
242 <150> PRIOR APPLICATION NUMBER: 60/103678
243 <151> PRIOR FILING DATE: 1998-10-08
245 <150> PRIOR APPLICATION NUMBER: 60/103679
246 <151> PRIOR FILING DATE: 1998-10-08
248 <150> PRIOR APPLICATION NUMBER: 60/103711
249 <151> PRIOR FILING DATE: 1998-10-08
251 <150> PRIOR APPLICATION NUMBER: 60/104257
252 <151> PRIOR FILING DATE: 1998-10-14
254 <150> PRIOR APPLICATION NUMBER: 60/104987
255 <151> PRIOR FILING DATE: 1998-10-20
257 <150> PRIOR APPLICATION NUMBER: 60/105000
258 <151> PRIOR FILING DATE: 1998-10-20
260 <150> PRIOR APPLICATION NUMBER: 60/105002
261 <151> PRIOR FILING DATE: 1998-10-20
263 <150> PRIOR APPLICATION NUMBER: 60/105104
264 <151> PRIOR FILING DATE: 1998-10-21
266 <150> PRIOR APPLICATION NUMBER: 60/105169
267 <151> PRIOR FILING DATE: 1998-10-22
269 <150> PRIOR APPLICATION NUMBER: 60/105266
270 <151> PRIOR FILING DATE: 1998-10-22
272 <150> PRIOR APPLICATION NUMBER: 60/105693
273 <151> PRIOR FILING DATE: 1998-10-26
275 <150> PRIOR APPLICATION NUMBER: 60/105694
276 <151> PRIOR FILING DATE: 1998-10-26
278 <150> PRIOR APPLICATION NUMBER: 60/105807
279 <151> PRIOR FILING DATE: 1998-10-27
281 <150> PRIOR APPLICATION NUMBER: 60/105881
282 <151> PRIOR FILING DATE: 1998-10-27
284 <150> PRIOR APPLICATION NUMBER: 60/105882

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/006,130

DATE: 12/17/2001

TIME: 11:12:13

Input Set : A:\Seq_List_for_P2830PlC7.wpd

Output Set: N:\CRF3\12172001\J006130.raw

285 <151> PRIOR FILING DATE: 1998-10-27
287 <150> PRIOR APPLICATION NUMBER: 60/106023
288 <151> PRIOR FILING DATE: 1998-10-28
290 <150> PRIOR APPLICATION NUMBER: 60/106029
291 <151> PRIOR FILING DATE: 1998-10-28
293 <150> PRIOR APPLICATION NUMBER: 60/106030
294 <151> PRIOR FILING DATE: 1998-10-28
296 <150> PRIOR APPLICATION NUMBER: 60/106032
297 <151> PRIOR FILING DATE: 1998-10-28
299 <150> PRIOR APPLICATION NUMBER: 60/106033
300 <151> PRIOR FILING DATE: 1998-10-28
302 <150> PRIOR APPLICATION NUMBER: 60/106062
303 <151> PRIOR FILING DATE: 1998-10-27
305 <150> PRIOR APPLICATION NUMBER: 60/106178
306 <151> PRIOR FILING DATE: 1998-10-28
308 <150> PRIOR APPLICATION NUMBER: 60/106248
309 <151> PRIOR FILING DATE: 1998-10-29
311 <150> PRIOR APPLICATION NUMBER: 60/106384
312 <151> PRIOR FILING DATE: 1998-10-29
314 <150> PRIOR APPLICATION NUMBER: 60/108500
315 <151> PRIOR FILING DATE: 1998-10-29
317 <150> PRIOR APPLICATION NUMBER: 60/106464
318 <151> PRIOR FILING DATE: 1998-10-30
320 <150> PRIOR APPLICATION NUMBER: 60/106856
321 <151> PRIOR FILING DATE: 1998-11-03
323 <150> PRIOR APPLICATION NUMBER: 60/106902
324 <151> PRIOR FILING DATE: 1998-11-03
326 <150> PRIOR APPLICATION NUMBER: 60/106905
327 <151> PRIOR FILING DATE: 1998-11-03
329 <150> PRIOR APPLICATION NUMBER: 60/106919
330 <151> PRIOR FILING DATE: 1998-11-03
332 <150> PRIOR APPLICATION NUMBER: 60/106932
333 <151> PRIOR FILING DATE: 1998-11-03
335 <150> PRIOR APPLICATION NUMBER: 60/106934
336 <151> PRIOR FILING DATE: 1998-11-03
338 <150> PRIOR APPLICATION NUMBER: 60/107783
339 <151> PRIOR FILING DATE: 1998-11-10
341 <150> PRIOR APPLICATION NUMBER: 60/108775
342 <151> PRIOR FILING DATE: 1998-11-17
344 <150> PRIOR APPLICATION NUMBER: 60/108779
345 <151> PRIOR FILING DATE: 1998-11-17
347 <150> PRIOR APPLICATION NUMBER: 60/108787
348 <151> PRIOR FILING DATE: 1998-11-17
350 <150> PRIOR APPLICATION NUMBER: 60/108788
351 <151> PRIOR FILING DATE: 1998-11-17
353 <150> PRIOR APPLICATION NUMBER: 60/108801
354 <151> PRIOR FILING DATE: 1998-11-17
356 <150> PRIOR APPLICATION NUMBER: 60/108802
357 <151> PRIOR FILING DATE: 1998-11-17

10/006,130 6

<210> 375
<211> 1098

<212> DNA

<213> Artificial

see item 11 on Error Summary Sheet

<400> 375

PSK →

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/006,130

DATE: 12/17/2001

TIME: 11:12:14

Input Set : A:\Seq_List_for_P2830P1C7.wpd

Output Set: N:\CRF3\12172001\J006130.raw

L:23 M:270 C: Current Application Number differs, Replaced Current Application No
 L:23 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:520 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
 L:523 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
 L:533 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
 L:536 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
 L:681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
 L:1342 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
 L:1345 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
 L:1355 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
 L:1358 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
 L:1368 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
 L:1371 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
 L:1551 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
 L:1554 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
 L:1564 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
 L:1567 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
 L:1577 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
 L:1580 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
 L:1911 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
 L:1914 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
 L:1924 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
 L:1927 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
 L:1937 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
 L:1940 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
 L:2406 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
 L:2409 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
 L:2419 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35
 L:2422 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
 L:2432 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:36
 L:2435 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
 L:2445 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:37
 L:2448 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
 L:2458 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38
 L:2461 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38
 L:2471 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39
 L:2474 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39
 L:2779 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:44
 L:2782 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44
 L:2792 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:45
 L:2795 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45
 L:2805 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:46
 L:2808 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:46
 L:2818 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47
 L:2821 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:47
 L:2831 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:48
 L:2834 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48
 L:3957 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:59

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/006,130

DATE: 12/17/2001

TIME: 11:12:14

Input Set : A:\Seq_List_for_P2830P1C7.wpd

Output Set: N:\CRF3\12172001\J006130.raw

L:3960 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:59
 L:3970 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:60
 L:3973 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:60
 L:3983 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:61
 L:3986 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:61
 L:4030 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
 L:4122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
 L:4158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
 L:4185 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:64
 L:4188 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:64
 L:4198 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:65
 L:4201 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:65
 L:4211 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:66
 L:4214 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:66
 L:4694 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:73
 L:4697 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:73
 L:4707 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:74
 L:4710 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:74
 L:4720 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:75
 L:4723 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:75
 L:5092 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:80
 L:5095 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:80
 L:5108 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:81
 L:5118 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:82
 L:5121 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:82
 L:5881 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:89
 L:5884 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:89
 L:5894 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:90
 L:5897 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:90
 L:5907 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:91
 L:5910 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:91
 L:5920 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:92
 L:5923 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:92
 L:5933 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:93
 L:5936 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:93
 L:6143 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:96
 L:6146 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:96
 L:6156 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:97
 L:6159 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:97
 L:6169 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:98
 L:6172 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:98
 L:6884 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:105
 L:6887 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:105
 L:6897 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:106
 L:6900 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:106
 L:6910 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:107
 L:6913 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:107
 L:6923 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:108
 L:6926 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:108

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/006,130

DATE: 12/17/2001

TIME: 11:12:14

Input Set : A:\Seq_List_for_P2830PlC7.wpd

Output Set: N:\CRF3\12172001\J006130.raw

L:6936 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:109
L:6939 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:109
L:7066 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:112
L:7069 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:112
L:7079 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:113
L:7082 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:113
L:7092 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:114
L:7095 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:114
L:7473 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:119
L:14262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:259
L:20824 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:20824 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:20939 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:377
L:22554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:422

1	5	10	15
Cys Phe Lys Ser Val	Leu Leu Ile Tyr Thr	Phe Ile Phe Trp	Ile
20	25		30
Thr Gly Val Ile	Leu Leu Ala Val Gly	Ile Trp Gly Lys Val	Ser
35	40		45
Leu Glu Asn Tyr Phe	Ser Leu Leu Asn Glu	Lys Ala Thr Asn	Val
50	55		60
Pro Phe Val Leu Ile	Ala Thr Gly Thr Val	Ile Ile Leu Leu	Gly
65	70		75
Thr Phe Gly Cys Phe	Ala Thr Cys Arg Ala	Ser Ala Trp Met	Leu
80	85		90
Lys Leu Tyr Ala Met	Phe Leu Thr Leu Val	Phe Leu Val Glu	Leu
95	100		105
Val Ala Ala Ile Val	Gly Phe Val Phe Arg	His Glu Ile Lys	Asn
110	115		120
Ser Phe Lys Asn Asn	Tyr Glu Lys Ala Leu	Lys Gln Tyr Asn	Ser
125	130		135
Thr Gly Asp Tyr Arg	Ser His Ala Val Asp	Lys Ile Gln Asn	Thr
140	145		150
Leu His Cys Cys Gly	Val Thr Asp Tyr Arg	Asp Trp Thr Asp	Thr
155	160		165
Asn Tyr Tyr Ser Glu	Lys Gly Phe Pro Lys	Ser Cys Cys Lys	Leu
170	175		180
Glu Asp Cys Thr Pro	Gln Arg Asp Ala Asp	Lys Val Asn Asn	Glu
185	190		195
Gly Cys Phe Ile Lys	Val Met Thr Ile Ile	Glu Ser Glu Met	Gly
200	205		210
Val Val Ala Gly Ile	Ser Phe Gly Val Ala	Cys Phe Gln Leu	Ile
215	220		225
Gly Ile Phe Leu Ala	Tyr Cys Xaa Ser Arg	Ala Ile Thr Asn	Asn
230	235		240
Gln Tyr Glu Ile Val			
245			

<210> 5

<211> 1218

<212> DNA

<213> Homo sapiens

<400> 5

cccacgcgtc cggcgccgtg gcctcgcgtc catctttgcc gttctctcgg 50

acctgtcaca aaggagtcgc gccgccgccg ccgccccctc cctccggtgg 100
 gcccgaggagg tagagaaagt cagtgccaca gcccgaccgc gctgctctga 150
 gccctgggca cgcggaacgg gagggagtct gagggttggg gacgtctgtg 200
 agggagggga acagccgctc gagcctgggg cgggcggacc ggactggggc 250
 cggggtaggc tctggaagg gcccgggaga gaggtggcgt tggtcagaac 300
 ctgagaaaca gccgagaggt tttccaccga ggcccgcgct tgagggatct 350
 gaagaggttc ctagaagagg gtgttcctc tttcgggggt cctcaccaga 400
 agaggttctt gggggtcgcc cttctgagga ggctgcggct aacagggccc 450
 agaactgcc a ttgatgtcc agaatcccct gtagttgata atgttgggaa 500
 taagctctgc aactttcttt ggcattcagt tgtaaaaaac aaataggatg 550
 caaatctctc aactccaggt tatgaaaaca gtacttgaa aactgaaaac 600
 tacctaaatg atcgtctttg gttggggcgt gttcttagcg agcagaagcc 650
 ttggccaggg tctgttggtg actctcgaag agcacatagc ccacttccta 700
 gggactggag gtgccgtac taccatgggt aattcctgta tctgccgaga 750
 tgacagtgga acagatgaca gtgttgacac ccaacagcaa caggccgaga 800
 acagtgcagt acccactgct gacacaagga gcccaaccacg ggaccctgtt 850
 cggccaccaa ggagggggcg aggacctcat gagccaagga gaaagaaaca 900
 aaatgtggat gggctagtgt tggacacact ggcagtaata cggactcttg 950
 tagataagta agtatctgac tcacggtcac ctccagtgga atgaaaagtg 1000
 ttctgcccgg aacctgact ttaggactcc ttcagttcct ttaggacata 1050
 ctgccaaagc cttgtgctca cagggcaaag gagaataatt taatgctccg 1100
 ctgatggcag agtaaatgat aagatttgat gtttttgctt gctgtcatct 1150
 actttgtctg gaaatgtcta aatgtttctg tagcagaaaa cacgataaag 1200
 ctatgatctt tattagag 1218

<210> 6

<211> 117

<212> PRT

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 1-16

<223> Signal Peptide

1	5	10	15
Cys Phe Lys Ser Val	Leu Leu Ile Tyr	Thr Phe Ile Phe Trp	Ile
20		25	30
Thr Gly Val Ile Leu	Leu Ala Val Gly	Ile Trp Gly Lys Val	Ser
35		40	45
Leu Glu Asn Tyr Phe	Ser Leu Leu Asn	Glu Lys Ala Thr Asn	Val
50		55	60
Pro Phe Val Leu Ile	Ala Thr Gly Thr	Val Ile Ile Leu Leu	Gly
65		70	75
Thr Phe Gly Cys Phe	Ala Thr Cys Arg	Ala Ser Ala Trp Met	Leu
80		85	90
Lys Leu Tyr Ala Met	Phe Leu Thr Leu	Val Phe Leu Val Glu	Leu
95		100	105
Val Ala Ala Ile Val	Gly Phe Val Phe	Arg His Glu Ile Lys	Asn
110		115	120
Ser Phe Lys Asn Asn	Tyr Glu Lys Ala	Leu Lys Gln Tyr Asn	Ser
125		130	135
Thr Gly Asp Tyr Arg	Ser His Ala Val	Asp Lys Ile Gln Asn	Thr
140		145	150
Leu His Cys Cys Gly	Val Thr Asp Tyr	Arg Asp Trp Thr Asp	Thr
155		160	165
Asn Tyr Tyr Ser Glu	Lys Gly Phe Pro	Lys Ser Cys Cys Lys	Leu
170		175	180
Glu Asp Cys Thr Pro	Gln Arg Asp Ala	Asp Lys Val Asn Asn	Glu
185		190	195
Gly Cys Phe Ile Lys	Val Met Thr Ile	Ile Glu Ser Glu Met	Gly
200		205	210
Val Val Ala Gly Ile	Ser Phe Gly Val	Ala Cys Phe Gln Leu	Ile
215		220	225
Gly Ile Phe Leu Ala	Tyr Cys Xaa Ser	Arg Ala Ile Thr Asn	Asn
230		235	240
Gln Tyr Glu Ile Val			
245			

<210> 5
 <211> 1218
 <212> DNA
 <213> Homo sapiens

<400> 5
 cccacgcgtc cggcgccgtg gcctcgcgtc catctttgcc gttctctcgg 50

acctgtcaca aaggagtcgc gccgccgccg ccgccccctc cctccggtgg 100
 gcccgaggagg tagagaaagt cagtgccaca gcccgaccgc gctgctctga 150
 gccctgggca cgcggaacgg gagggagtct gagggttggg gacgtctgtg 200
 agggagggga acagccgctc gagcctgggg cgggcggacc ggactggggc 250
 cggggtaggc tctggaaagg gcccgggaga gaggtggcgt tggtcagaac 300
 ctgagaaaca gccgagaggt tttccaccga ggcccgcgct tgagggatct 350
 gaagaggttc ctagaagagg gtgttcctc tttcgggggt cctcaccaga 400
 agaggttctt gggggtcgcc cttctgagga ggctgcggct aacagggccc 450
 agaactgcca ttggatgtcc agaatccct gtagttgata atgttgggaa 500
 taagctctgc aactttcttt ggcattcagt tgttaaaaac aaataggatg 550
 caaattcctc aactccaggt tatgaaaaca gtacttggaa aactgaaaac 600
 tacctaaatg atcgtctttg gttgggccgt gttcttagcg agcagaagcc 650
 ttggccaggg tctgttggtg actctcgaag agcacatagc ccacttccta 700
 gggactggag gtgccgtac taccatgggt aattcctgta tctgccgaga 750
 tgacagtga acagatgaca gtgttgacac ccaacagcaa caggccgaga 800
 acagtgcagt acccactgct gacacaagga gccaaccacg ggaccctgtt 850
 cggccaccaa ggagggggcg aggacctcat gagccaagga gaaagaaaca 900
 aaatgtggat gggctagtgt tggacacact ggcagtaata cggactcttg 950
 tagataagta agtatctgac tcacggtcac ctccagtga atgaaaagtg 1000
 ttctgcccgg aaccatgact ttaggactcc ttcagttcct ttaggacata 1050
 ctgccaaagc cttgtgctca cagggcaaag gagaataatt taatgctccg 1100
 ctgatggcag agtaaagtat aagatttgat gtttttgctt gctgtcatct 1150
 actttgtctg gaaatgtcta aatgtttctg tagcagaaaa cacgataaag 1200
 ctatgatctt tattagag 1218

<210> 6

<211> 117

<212> PRT

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 1-16

<223> Signal Peptide

<220>
 <221> misc feature
 <222> 18-24, 32-38, 34-40, 35-41, 51-57
 <223> N-Myristoylation Site.

<220>
 <221> misc feature
 <222> 22-26, 50-54, 113-117
 <223> Casein Kinase II Phosphorylation Site.

<400> 6
 Met Ile Val Phe Gly Trp Ala Val Phe Leu Ala Ser Arg Ser Leu
 1 5 10 15
 Gly Gln Gly Leu Leu Leu Thr Leu Glu Glu His Ile Ala His Phe
 20 25 30
 Leu Gly Thr Gly Gly Ala Ala Thr Thr Met Gly Asn Ser Cys Ile
 35 40 45
 Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln
 50 55 60
 Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp Thr Arg Ser
 65 70 75
 Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg Gly Pro
 80 85 90
 His Glu Pro Arg Arg Lys Lys Gln Asn Val Asp Gly Leu Val Leu
 95 100 105
 Asp Thr Leu Ala Val Ile Arg Thr Leu Val Asp Lys
 110 115

<210> 7
 <211> 756
 <212> DNA
 <213> Homo sapiens

<400> 7
 ggcacgaggc gctgtccacc cgggggcgtg ggagtgaggt accagattca 50
 gcccatattgg ccccgacgcc tctgttctcg gaatccgggt gctgcggatt 100
 gaggtcccgg ttcctaacgg actgcaagat ggaggaaggc gggaacctag 150
 gaggcctgat taagatggtc catctactgg tcttgtcagg tgcctggggc 200
 atgcaaatgt ggggtgacct cgtctcaggc ttctgtcttt tccgaagcct 250
 tccccgacat accttcggac tagtgcagag caaactcttc cccttctact 300
 tccacatctc catgggctgt gccttcatca acctctgcat cttggcttca 350
 cagcatgctt gggctcagct cacattctgg gaggccagcc agctttacct 400
 gctgttcttg agccttacgc tggccactgt caacgcccgc tggettggaac 450

cccgcaccac agctgccatg tgggccctgc aaaccgtgga gaaggagcga 500
 ggcctgggtg gggaggtacc aggagccac caggggtcccg atccctaccg 550
 ccagctgcga gagaaggacc ccaagtacag tgctctccgc cagaatttct 600
 tccgctacca tgggctgtcc tctctttgca atctgggctg cgtcctgagc 650
 aatgggctct gtctcgctgg ccttgccctg gaaataagga gcctctagca 700
 tgggccctgc atgctaataa atgcttcttc agaaatgaaa aaaaaaaaaa 750
 aaaaaa 756

<210> 8
 <211> 189
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-24
 <223> Signal Peptide

<220>
 <221> misc_feature
 <222> 4-10, 5-11, 47-53, 170-176, 176-182
 <223> N-Myristoylation Site.

<220>
 <221> misc_feature
 <222> 44-85
 <223> G-protein Coupled Receptors Proteins.

<220>
 <221> misc_feature
 <222> 54-65
 <223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

<220>
 <221> misc_feature
 <222> 82-86
 <223> Casein Kinase II Phosphorylation Site.

<220>
 <221> TRANSMEM
 <222> 86-103, 60-75
 <223> Transmembrane Domain

<220>
 <221> misc_feature
 <222> 144-151
 <223> Tyrosine Kinase Phosphorylation Site.

<400> 8
 Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His
 1 5 10 15

Leu	Leu	Val	Leu	Ser	Gly	Ala	Trp	Gly	Met	Gln	Met	Trp	Val	Thr	20	25	30
Phe	Val	Ser	Gly	Phe	Leu	Leu	Phe	Arg	Ser	Leu	Pro	Arg	His	Thr	35	40	45
Phe	Gly	Leu	Val	Gln	Ser	Lys	Leu	Phe	Pro	Phe	Tyr	Phe	His	Ile	50	55	60
Ser	Met	Gly	Cys	Ala	Phe	Ile	Asn	Leu	Cys	Ile	Leu	Ala	Ser	Gln	65	70	75
His	Ala	Trp	Ala	Gln	Leu	Thr	Phe	Trp	Glu	Ala	Ser	Gln	Leu	Tyr	80	85	90
Leu	Leu	Phe	Leu	Ser	Leu	Thr	Leu	Ala	Thr	Val	Asn	Ala	Arg	Trp	95	100	105
Leu	Glu	Pro	Arg	Thr	Thr	Ala	Ala	Met	Trp	Ala	Leu	Gln	Thr	Val	110	115	120
Glu	Lys	Glu	Arg	Gly	Leu	Gly	Gly	Glu	Val	Pro	Gly	Ser	His	Gln	125	130	135
Gly	Pro	Asp	Pro	Tyr	Arg	Gln	Leu	Arg	Glu	Lys	Asp	Pro	Lys	Tyr	140	145	150
Ser	Ala	Leu	Arg	Gln	Asn	Phe	Phe	Arg	Tyr	His	Gly	Leu	Ser	Ser	155	160	165
Leu	Cys	Asn	Leu	Gly	Cys	Val	Leu	Ser	Asn	Gly	Leu	Cys	Leu	Ala	170	175	180
Gly	Leu	Ala	Leu	Glu	Ile	Arg	Ser	Leu							185		

<210> 9
 <211> 1508
 <212> DNA
 <213> Homo sapiens

<400> 9
 aattcagatt ttaagcccat tctgcagtgg aatttcatga actagcaaga 50
 ggacaccatc ttcttgtatt atacaagaaa ggagtgtacc tatcacacac 100
 agggggaaaa atgctctttt gggtgctagg cctcctaata ctctgtgggt 150
 ttctgtggac tcgtaaagga aaactaaaga ttgaagacat cactgataag 200
 tacattttta tcaactggatg tgactcgggc tttggaaaact tggcagccag 250
 aacttttgat aaaaagggat ttcattgaat cgctgcctgt ctgactgaat 300
 caggatcaac agcttttaaag gcagaaacct cagagagact tcgtactgtg 350
 cttctggatg tgaccgaccc agagaatgtc aagaggactg cccagtgggt 400

gaagaaccaa gttggggaga aaggtctctg gggctctgac aataatgctg 450
 gtgttcccg cgtgctggct cccactgact ggctgacact agaggactac 500
 agagaaccta ttgaagtga cctgtttgga ctcatcagtg tgacactaaa 550
 tatgcttcct ttggtcaaga aagctcaagg gagagttatt aatgtctcca 600
 gtgttgagg tgccttgca atcgttgag ggggtatac tccatccaaa 650
 tatgcagtg aaggtttcaa tgacagctta agacgggaca tgaaagcttt 700
 tgggtgacac gtctcatgca ttgaaccagg attgttcaaa aaaaacttg 750
 cagatccagt aaaggttaatt gaaaaaaaaac tcgccatttg ggagcagctg 800
 tctccagaca tcaaacaaca atatggagaa ggttacattg aaaaaagtct 850
 agacaaactg aaaggcaata aatcctatgt gaacatggac ctctctccg 900
 tggtagagt catggaccac gctctaaca gtctcttccc taagactcat 950
 tatgccgctg gaaaagatgc caaaattttc tggatacctc tgtctcacat 1000
 gccagcagct ttgcaagact ttttattgtt gaaacagaaa gcagagctgg 1050
 ctaatcccaa ggcagtgtga ctgagctaac cacaatgtc tcctccaggc 1100
 tatgaaattg gccgatttca agaacacatc tccttttcaa cccatttct 1150
 tatctgctcc aacctggact catttagatc gtgcttattt ggattgcaaa 1200
 agggagtccc accatcgtg gtggtatccc aggtccctg ctcaagtttt 1250
 ctttgaaaag gagggctgga atggtacatc acataggcaa gtcctgccct 1300
 gtatttaggc ttgctgct tgggtgatg taagggaat tgaaagactt 1350
 gccattcaa aatgatcttt accgtggcct gcccattgct tatgggtccc 1400
 agcatttaca gtaacttgat aatgttaagt atcatctctt atctaaatat 1450
 taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaa 1508

<210> 10

<211> 319

<212> PRT

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 1-17

<223> Signal Peptide

<220>

<221> misc_feature

<222> 36-47, 108-113, 166-171,198-203, 207-212
 <223> N-myristoylation Sites.

<220>
 <221> misc_feature
 <222> 39-42
 <223> Glycosaminoglycan Attachment Site.

<220>
 <221> TRANSMEM
 <222> 136-152
 <223> Transmembrane Domain

<220>
 <221> misc_feature
 <222> 161-163, 187-190 and 253-256
 <223> N-glycosylation Sites.

<400> 10
 Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu
 1 5 10 15
 Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
 20 25 30
 Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
 35 40 45
 Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
 50 55 60
 Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
 65 70 75
 Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
 80 85 90
 Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
 95 100 105
 Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
 110 115 120
 Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu
 125 130 135
 Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro
 140 145 150
 Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
 155 160 165
 Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys
 170 175 180
 Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys
 185 190 195

Ala	Phe	Gly	Val	His	Val	Ser	Cys	Ile	Glu	Pro	Gly	Leu	Phe	Lys
				200					205					210
Thr	Asn	Leu	Ala	Asp	Pro	Val	Lys	Val	Ile	Glu	Lys	Lys	Leu	Ala
				215					220					225
Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu
				230					235					240
Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser
				245					250					255
Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His
				260					265					270
Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys
				275					280					285
Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala
				290					295					300
Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn
				305					310					315

Pro Lys Ala Val

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapiens

<400> 11
 gcgggctgtt gacggcgctg cgatggctgc ctgcgagggc aggagaagcg 50
 gagctctcgg ttcctctcag tcggacttcc tgacgccgcc agtgggcggg 100
 gcccttgagg ccgtgccac cactgtagtc atgtaccac cgccgccgcc 150
 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttctcc ttgcctttct 300
 gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400
 ggggttaaac cagcaaatcc acccgtctta ccagctcctc agaaggcgga 450
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600
 ggatccccgc ccggaaggag atccgcagag gacagtcac agctggaggg 650

gagcggatgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700
gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750
agtgcacatg aactatcgcc agaagggcgt gattgacgtc ttcctgcatg 800
catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850
gtgtccagggt ccttcagtga gtggtttggc ctcggtctca cactgatcga 900
cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950
ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgtc 1000
aacctgtttg agagcacgat ccgcatcctg ggggggctcc tgagtgccta 1050
ccacctgtct ggggacagcc tcttcctgag gaaagctgag gattttggaa 1100
atcggctaata gcctgccttc agaaccacat ccaagattcc ttactcggat 1150
gtgaacatcg gtactggagt tgcccaccg ccacgggtgga cctccgacag 1200
cactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250
gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300
cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350
caatacccac agtggcctct tcaccacact gggcgtattc acgctgggag 1400
ccagggccga cagctactat gagtacctgc tgaagcagtg gatccagggc 1450
gggaagcagg agacacagct gctggaagac tacgtggaag ccatcgaggg 1500
tgtcagaacg cacctgctgc ggcactccga gccagtaag ctacaccttg 1550
tgggggagct tgcccacggc cgcttcagtg ccaagatgga ccacctggtg 1600
tgcttctctg cagggacgct ggctctgggc gtctaccacg gcctgcccgc 1650
cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700
accggcagat ggagacgggg ctgagtcccg agatcgtgca cttcaacctt 1750
tacccccagc cgggccgtcg ggacgtggag gtcaagccag cagacaggca 1800
caacctgctg cggccagaga ccgtggagag cctgttctac ctgtaccgag 1850
tcacagggga ccgcaaatac caggactggg gctgggagat tctgcagagc 1900
ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950
tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000
tcctggggga gacgctcaag tatctgttct tgctcttctc cgatgaccca 2050
aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccaccctct 2100

gcctatctgg acccctgcct aggggtggatg gctgctggtg tggggacttc 2150
 ggggtgggcag aggcaccttg ctgggtctgt ggcattttcc aaggggccac 2200
 gtagcaccgg caaccgcaa gtggcccagg ctctgaactg gctctgggct 2250
 cctcctcgtc tctgctttaa tcaggacacc gtgaggacaa gtgaggccgt 2300
 cagtcttggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350
 ttctccaga agacacgaat catgactcac gattgctgaa gcctgagcag 2400
 gtctctgtgg gccgaccaga ggggggcttc gaggtggtcc ctggtactgg 2450
 ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctcgtgaagc 2500
 ctcagatgtc cccaatccaa gggctctggag gggctgccgt gactccagag 2550
 gcctgagget ccagggctgg ctctggtgtt tacaagctgg actcagggat 2600
 cctcctggcc gcccgcagg gggcttggag ggctggacgg caagtccgtc 2650
 tagctcacgg gccctccag tggaatgggt cttttcgggtg gagataaaag 2700
 ttgatttgct ctaaccgcaa 2720

<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

Met	Ala	Ala	Cys	Glu	Gly	Arg	Arg	Ser	Gly	Ala	Leu	Gly	Ser	Ser	1	5	10	15
Gln	Ser	Asp	Phe	Leu	Thr	Pro	Pro	Val	Gly	Gly	Ala	Pro	Trp	Ala	20	25	30	
Val	Ala	Thr	Thr	Val	Val	Met	Tyr	Pro	Pro	Pro	Pro	Pro	Pro	Pro	35	40	45	
His	Arg	Asp	Phe	Ile	Ser	Val	Thr	Leu	Ser	Phe	Gly	Glu	Ser	Tyr	50	55	60	
Asp	Asn	Ser	Lys	Ser	Trp	Arg	Arg	Arg	Ser	Cys	Trp	Arg	Lys	Trp	65	70	75	
Lys	Gln	Leu	Ser	Arg	Leu	Gln	Arg	Asn	Met	Ile	Leu	Phe	Leu	Leu	80	85	90	
Ala	Phe	Leu	Leu	Phe	Cys	Gly	Leu	Leu	Phe	Tyr	Ile	Asn	Leu	Ala	95	100	105	

Asp His Trp Lys	Ala Leu Ala Phe Arg	Leu Glu Glu Glu Gln Lys	110	115	120
Met Arg Pro Glu	Ile Ala Gly Leu Lys	Pro Ala Asn Pro Pro Val	125	130	135
Leu Pro Ala Pro	Gln Lys Ala Asp Thr	Asp Pro Glu Asn Leu Pro	140	145	150
Glu Ile Ser Ser	Gln Lys Thr Gln Arg	His Ile Gln Arg Gly Pro	155	160	165
Pro His Leu Gln	Ile Arg Pro Pro Ser	Gln Asp Leu Lys Asp Gly	170	175	180
Thr Gln Glu Glu	Ala Thr Lys Arg Gln	Glu Ala Pro Val Asp Pro	185	190	195
Arg Pro Glu Gly	Asp Pro Gln Arg Thr	Val Ile Ser Trp Arg Gly	200	205	210
Ala Val Ile Glu	Pro Glu Gln Gly Thr	Glu Leu Pro Ser Arg Arg	215	220	225
Ala Glu Val Pro	Thr Lys Pro Pro Leu	Pro Pro Ala Arg Thr Gln	230	235	240
Gly Thr Pro Val	His Leu Asn Tyr Arg	Gln Lys Gly Val Ile Asp	245	250	255
Val Phe Leu His	Ala Trp Lys Gly Tyr	Arg Lys Phe Ala Trp Gly	260	265	270
His Asp Glu Leu	Lys Pro Val Ser Arg	Ser Phe Ser Glu Trp Phe	275	280	285
Gly Leu Gly Leu	Thr Leu Ile Asp Ala	Leu Asp Thr Met Trp Ile	290	295	300
Leu Gly Leu Arg	Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val Ser	305	310	315
Lys Lys Leu His	Phe Glu Lys Asp Val	Asp Val Asn Leu Phe Glu	320	325	330
Ser Thr Ile Arg	Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His Leu	335	340	345
Ser Gly Asp Ser	Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly Asn	350	355	360
Arg Leu Met Pro	Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr Ser	365	370	375
Asp Val Asn Ile	Gly Thr Gly Val Ala	His Pro Pro Arg Trp Thr	380	385	390
Ser Asp Ser Thr	Val Ala Glu Val Thr	Ser Ile Gln Leu Glu Phe			

395					400					405				
Arg	Glu	Leu	Ser	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala
				410					415					420
Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys
				425					430					435
Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe
				440					445					450
Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr
				455					460					465
Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu
				470					475					480
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg
				485					490					495
Thr	His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val
				500					505					510
Gly	Glu	Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu
				515					520					525
Val	Cys	Phe	Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly
				530					535					540
Leu	Pro	Ala	Ser	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr
				545					550					555
Cys	Tyr	Gln	Met	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu
				560					565					570
Ile	Val	His	Phe	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val
				575					580					585
Glu	Val	Lys	Pro	Ala	Asp	Arg	His	Asn	Leu	Leu	Arg	Pro	Glu	Thr
				590					595					600
Val	Glu	Ser	Leu	Phe	Tyr	Leu	Tyr	Arg	Val	Thr	Gly	Asp	Arg	Lys
				605					610					615
Tyr	Gln	Asp	Trp	Gly	Trp	Glu	Ile	Leu	Gln	Ser	Phe	Ser	Arg	Phe
				620					625					630
Thr	Arg	Val	Pro	Ser	Gly	Gly	Tyr	Ser	Ser	Ile	Asn	Asn	Val	Gln
				635					640					645
Asp	Pro	Gln	Lys	Pro	Glu	Pro	Arg	Asp	Lys	Met	Glu	Ser	Phe	Phe
				650					655					660
Leu	Gly	Glu	Thr	Leu	Lys	Tyr	Leu	Phe	Leu	Leu	Phe	Ser	Asp	Asp
				665					670					675
Pro	Asn	Leu	Leu	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr	Glu	Ala
				680					685					690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggctct tcagtgaagt gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
ggcgccgcgt aggcccgga ggccgggccc gccgggctgc gagcgccctgc 50
cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gaggaagcg 100
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150
ccctcggaag tggtccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300
 cccccagag cgcacctg agcactggga agaagacgca tcctggggcc 350
 cccaccgctt ggcagtgtg gtgcccttcc gcgaacgctt cgaggagctc 400
 ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450
 gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500
 cagcgctcat caacgtgggc ttcttgaga gcagcaacag cacggactac 550
 attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600
 tggctttcct gaggtgagg ccttcacgt ggcctccccg gagctccacc 650
 ctctctacca ctacaagacc tatgtcggcg gcatcctgct gctctccaag 700
 cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750
 ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800
 ttttcgccc ctcgggaatc acaactgggt acaagacatt tcgccacctg 850
 catgaccag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900
 acaggagcag ttcaaggtgg acaggaggagg aggcctgaac actgtgaagt 950
 accatgtggc ttcccgact gccctgtctg tgggcggggc cccctgcact 1000
 gtcctcaaca tcatgttga ctgtgacaag accgccacac cctggtgcac 1050
 attcagctga gctggatgga cagtaggaa gcctgtacct acaggccata 1100
 ttgctcaggc tcaggacaag gcctcaggtc gtgggcccag ctctgacagg 1150
 atgtggagtg gccaggacca agacagcaag ctacgcaatt gcagccaccc 1200
 ggccgccaag gcaggcttgg gctgggccag gacacgtggg gtgcctggga 1250
 cgctgcttgc catgcacagt gatcagagag aggctggggg gtgtcctgtc 1300
 cgggaccccc cctgccttcc tgctcaccct actctgacct ccttcacgtg 1350
 cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400
 cctactctga cctccttcac gtgcccaggc ctgtgggtag tggggagggc 1450
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens
 <220>

<221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25, 65-71, 247-253, 285-291, 303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
 1 5 10 15
 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
 20 25 30
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
 50 55 60
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
 65 70 75
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
 80 85 90
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
 95 100 105
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
 110 115 120
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
 125 130 135
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

140										145					150				
Glu	Ser	Ser	Asn	Ser	Thr	Asp	Tyr	Ile	Ala	Met	His	Asp	Val	Asp					
				155					160					165					
Leu	Leu	Pro	Leu	Asn	Glu	Glu	Leu	Asp	Tyr	Gly	Phe	Pro	Glu	Ala					
				170					175					180					
Gly	Pro	Phe	His	Val	Ala	Ser	Pro	Glu	Leu	His	Pro	Leu	Tyr	His					
				185					190					195					
Tyr	Lys	Thr	Tyr	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ser	Lys	Gln	His					
				200					205					210					
Tyr	Arg	Leu	Cys	Asn	Gly	Met	Ser	Asn	Arg	Phe	Trp	Gly	Trp	Gly					
				215					220					225					
Arg	Glu	Asp	Asp	Glu	Phe	Tyr	Arg	Arg	Ile	Lys	Gly	Ala	Gly	Leu					
				230					235					240					
Gln	Leu	Phe	Arg	Pro	Ser	Gly	Ile	Thr	Thr	Gly	Tyr	Lys	Thr	Phe					
				245					250					255					
Arg	His	Leu	His	Asp	Pro	Ala	Trp	Arg	Lys	Arg	Asp	Gln	Lys	Arg					
				260					265					270					
Ile	Ala	Ala	Gln	Lys	Gln	Glu	Gln	Phe	Lys	Val	Asp	Arg	Glu	Gly					
				275					280					285					
Gly	Leu	Asn	Thr	Val	Lys	Tyr	His	Val	Ala	Ser	Arg	Thr	Ala	Leu					
				290					295					300					
Ser	Val	Gly	Gly	Ala	Pro	Cys	Thr	Val	Leu	Asn	Ile	Met	Leu	Asp					
				305					310					315					
Cys	Asp	Lys	Thr	Ala	Thr	Pro	Trp	Cys	Thr	Phe	Ser								
				320					325										

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 18
 gcgaacgctt cgaggagtcc tgg 23

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-24
<223> Synthetic construct

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50
aacgtgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
gactggtcgg tgcccagaaa gtctcttctg cactgacgc ccccatcagg 150
gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcacggcc 200
tgccatgacc tgcagccaag cccagccccg tggggaaggg gagaaagtgg 250
gggatggcta agaaagctgg gagatagggg acagaagagg gtagtgggtg 300
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
cctgtgttca atgtttgtaa agattgttct gtgtaaaat gtctttataa 450
taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15
Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30
Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45
Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60
Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

gggacccatg cggccgtgac ccccggtcc ctagaggccc agcgcagccg 50
cagcggacaa aggagcatgt ccgcgccggg gaaggcccg cctccggccg 100
ccataaggct cgggtcgccg ctggggccgc gccgcgctcc tgcccggccg 150
ggctccgggg cggcccgtta ggccagtgcg ccgcgcgtcg ccccgagggc 200
cccgcccgcc agcatggagc caccgggacg ccggcggggc cgcgcgagc 250
cgccgctgtt gctgccgtc tcgctgttag cgctgctgc gctgctggga 300
ggcggcgggc gggcgggcgc cgcggcgctg cccgccggct gcaagcacga 350
tgggcggccc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400
tgggtgtgag cagcctggaa ctgcgcagg tcctgcccgc agatactctg 450
cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500
gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550
gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600
tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650
agacatattt cgaggactca ccaatctggt tcggctaaac ctttcgggga 700
atttgttttc ttcattatct caaggaactt ttgattatct tgcgtcatta 750
cggctcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800
gtggatgcat cgctgggtaa aggagaagaa catcacggtg cgggatacca 850

ggtgtgttta tcctaagtca ctgcaggccc aaccagtcac aggcgtgaag 900
 caggagctgt tgacatgca cctccgctt gaattgccgt cttctacat 950
 gactccatct catcgccaag ttgtgtttga aggagacagc cttcctttcc 1000
 agtgcattgc ttcataatatt gatcaggaca tgcaagtgtt gtggtatcag 1050
 gatgggagaa tagttgaaac cgatgaatcg caaggtatct ttgttgaaaa 1100
 gaacatgatt cacaactgct ccttgattgc aagtgcccta accatttcta 1150
 atattcaggc tggatctact ggaaattggg gctgtcatgt ccagacccaa 1200
 cgtgggaata atacaggagc tgtggatatt gtggtattag agagttctgc 1250
 acagtactgt cctccagaga ggggtgtaaa caacaaaggt gacttcagat 1300
 ggcccagAAC attggcaggc attactgcat atctgcagtg tacgcggaac 1350
 acccatggca gtgggatata tcccggaaac ccacaggatg agagaaaagc 1400
 ttggcgcaga tgtgatagag gtggcttttg ggcagatgat gattattctc 1450
 gctgtcagta tgcaaatgat gtcactagag ttctttatat gtttaatcag 1500
 atgcccctca atcttaccaa tgccgtggca acagctcgac agttactggc 1550
 ttacactgtg gaagcagcca acttttctga caaaatggat gttatatttg 1600
 tggcagaaat gattgaaaaa tttggaagat ttaccaagga ggaaaaatca 1650
 aaagagctag gtgacgtgat ggttgacatt gcaagtaaca tcatgttggc 1700
 tgatgaacgt gtcctgtggc tggcgcagag ggaagctaaa gcctgcagta 1750
 ggattgtgca gtgtcttcag cgcattgcta cctaccggct agccggtgga 1800
 gctcacgttt attcaacata ttcacccaat attgctctgg aagcttatgt 1850
 catcaagtct actggcttca cggggatgac ctgtaccgtg ttccagaaag 1900
 tggcagcctc tgatcgtaca ggactttcgg attatgggag gcgggatcca 1950
 gagggaaacc tggataagca gctgagcttt aagtgcaatg tttcaaatac 2000
 attttcgagt ctggcactaa aggtatgtta cattctgcaa tcatttaaga 2050
 ctatttacag ttaaattaga atgctccaaa tgttctgctt cgcaaaataa 2100
 ccttattaaa agattttttt ttgcaggaag ataggtatta ttgcttttgc 2150
 tactgtttta aagaaaacta accaggaaga actgcattac gactttcaag 2200
 ggccctaggc atttttgcct ttgattccct ttcttcacat aaaaatatca 2250
 gaaattacat ttataactg cagtgtgata aatgcaaata tactattgtt 2300

acatgtgaaa aaattttatt tgacttaaaa gtttatttat ttgttttttt 2350
 gctcctgatt ttaagacaat aagatgtttt catgggcccc taaaagtatc 2400
 atgagccttt ggcaactgcg ctgccaagcc tagtggagaa gtcaaccctg 2450
 agaccaggtg tttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500
 acacaaatat gtcatatatc tttttttaaa aaaagtattt cattgaagca 2550
 agcaaaatga aagcattttt actgattttt aaaattggtg ctttagatat 2600
 atttgactac actgtattga agcaaataga ggaggcacia ctccagcacc 2650
 ctaatggaac cacatttttt tcacttagct ttctgtgggc atgtgtaatt 2700
 gtattctctg cggtttttaa tctcacagta ctttatttct gtcttgtccc 2750
 tcaataatat cacaaacaat attccagtca ttttaatggc tgcataataa 2800
 ctgatccaac aggtgttagg tgttctggtt tagtgtgagc actcaataaa 2850
 tattgaatga atgaacgaaa aaaaaaaaaa aaa 2883

<210> 24
 <211> 616
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-33
 <223> Signal peptide.

<220>
 <221> TRANSMEM
 <222> 13-40
 <223> Transmembrane domain (type II).

<400> 24
 Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu
 1 5 10 15
 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
 35 40 45
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
 50 55 60
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
 65 70 75
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
 80 85 90

Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser	
				95					100					105	
Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser	Ile	
				110					115					120	
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp	
				125					130					135	
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg	
				140					145					150	
Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe	
				155					160					165	
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg	
				170					175					180	
Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile	
				185					190					195	
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg	
				200					205					210	
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val	
				215					220					225	
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Glu	
				230					235					240	
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe	
				245					250					255	
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	
				260					265					270	
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu	
				275					280					285	
Thr	Asp	Glu	Ser	Gln	Gly	Ile	Phe	Val	Glu	Lys	Asn	Met	Ile	His	
				290					295					300	
Asn	Cys	Ser	Leu	Ile	Ala	Ser	Ala	Leu	Thr	Ile	Ser	Asn	Ile	Gln	
				305					310					315	
Ala	Gly	Ser	Thr	Gly	Asn	Trp	Gly	Cys	His	Val	Gln	Thr	Lys	Arg	
				320					325					330	
Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser	
				335					340					345	
Ala	Gln	Tyr	Cys	Pro	Pro	Glu	Arg	Val	Val	Asn	Asn	Lys	Gly	Asp	
				350					355					360	
Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln	
				365					370					375	
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro	

	380		385		390
Gln Asp Glu Arg	Lys Ala Trp Arg Arg	Cys Asp Arg Gly Gly	Phe		
	395	400	405		
Trp Ala Asp Asp	Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp	Val		
	410	415	420		
Thr Arg Val Leu	Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu	Thr		
	425	430	435		
Asn Ala Val Ala	Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val	Glu		
	440	445	450		
Ala Ala Asn Phe	Ser Asp Lys Met Asp	Val Ile Phe Val Ala	Glu		
	455	460	465		
Met Ile Glu Lys	Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser	Lys		
	470	475	480		
Glu Leu Gly Asp	Val Met Val Asp Ile	Ala Ser Asn Ile Met	Leu		
	485	490	495		
Ala Asp Glu Arg	Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys	Ala		
	500	505	510		
Cys Ser Arg Ile	Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr	Arg		
	515	520	525		
Leu Ala Gly Gly	Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn	Ile		
	530	535	540		
Ala Leu Glu Ala	Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly	Met		
	545	550	555		
Thr Cys Thr Val	Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr	Gly		
	560	565	570		
Leu Ser Asp Tyr	Gly Arg Arg Asp Pro	Glu Gly Asn Leu Asp	Lys		
	575	580	585		
Gln Leu Ser Phe	Lys Cys Asn Val Ser	Asn Thr Phe Ser Ser	Leu		
	590	595	600		
Ala Leu Lys Val	Cys Tyr Ile Leu Gln	Ser Phe Lys Thr Ile	Tyr		
	605	610	615		

Ser

<210> 25
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24

<223> Synthetic construct

<400> 25
gaggactcac caatctggtt cggc 24

<210> 26
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 26
aactggaaag gaaggctgtc tccc 24

<210> 27
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 27
gtaaaggaga agaacatcac ggtacgggat accaggtgtg tttatcctaa 50

<210> 28
<211> 683
<212> DNA
<213> Homo sapiens

<400> 28
gcgtggggat gtctaggagc tcgaagggtg tgctgggcct ctcggtgctg 50
ctgacggcgg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100
gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150
aaaaagaaaa cattcgtctt ttgggagaac agattatattt gactgagcaa 200
cttgaagcag aaagagagaa gatgttattg gcaaaaaggat ctcaaaaatc 250
atgacttgaa tgtgaaatat ctgttgga gacaacacga gtttgtgtgt 300
gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350
actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400
ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450
tttggaagag tctgtctggg tgatcctggt agaagcccca ttagggtcac 500
tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

ggaagggatg gatagtagca tccacctgag tagtctgatc agtcggcatg 600
 atgacgaagc caccagaaca tcgacctcag aaggactgga ggaaggtgaa 650
 gtggaggaggag agacgtcct gatcgtcgaa tcc 683

<210> 29
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-21
 <223> Signal peptide.

<400> 29
 Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu
 1 5 10 15
 Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
 20 25 30
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
 50 55 60
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
 65 70 75
 Lys Gly Ser Gln Lys Ser
 80

<210> 30
 <211> 2128
 <212> DNA
 <213> Homo sapiens

<400> 30
 ctgtcgtctt tgcttcagcc gcagtcgcca ctggctgcct gagtgctct 50
 tacagcctgt tccaagtgtg gcttaatccg tctccaccac cagatctttc 100
 tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggtaaccgc 150
 caccaccatc acaaccacca cgacgtcatc ttcgggcctg gggcccccca 200
 tgatcgtggg gtccccctcg gccctgacac agcccctggg tctccttcgc 250
 ctgctgcagc tgggtgtctac ctgcgtggcc ttctcgtctg tggctagcgt 300
 gggcgccctg acgggggtcca tgggcaactg gtccatgttc acctggtgct 350
 tctgcttctc cgtgaccctg atcactctca tcgtggagct gtgcgggctc 400
 caggcccgtt tccccctgtc ttggcgcaac ttccccatca ccttcgcctg 450

ctatgcggcc ctcttctgcc tctcggcctc catcatctac cccaccacct 500
 atgtccagtt cctgtccac gccggttcgc gggaccacgc catcgccgcc 550
 accttcttct cctgcatcgc gtgtgtggct tacgccaccg aagtggcctg 600
 gacccggggc cgccccggcg agatcactgg ctatatggcc accgtaccgc 650
 ggctgtgaa ggtgctggag accttcgttg cctgcatcat cttcgcgttc 700
 atcagcgacc ccaacctgta ccagcaccag ccggccctgg agtgggtgcgt 750
 ggcggtgtac gccatctgct tcatcctagc ggccatcgcc atcctgctga 800
 acctggggga gtgcaccaac gtgctacca tccccctccc cagcttcctg 850
 tcggggctgg ccttgctgtc tgtcctcctc tatgccaccg cccttggtct 900
 ctggccccct taccagttcg atgagaagta tggcgccag cctcggcgct 950
 cgagagatgt aagctgcagc cgcagccatg cctactacgt gtgtgcctgg 1000
 gaccgcccac tggtgtggc catcctgacg gccatcaacc tactggcgta 1050
 tgtggctgac ctggtgcact ctgcccacct ggtttttgtc aaggctaaag 1100
 actctcccaa gaggtcccg tccccctcc aacctcttg ttcttcttgc 1150
 ccgagttttc tttatggagt acttctttcc tccgcctttc ctctgttttc 1200
 ctcttctgt ctccccccc tcccacctt ttctttcctt cccaattcct 1250
 tgcactctaa ccagttcttg gatgcatctt ctccctccc ttctctcttg 1300
 ctgtttcctt cctgtgttg tttgttgccc acatcctgtt ttcacccctg 1350
 agctgtttct ctttttctt tctttcttt ttttttttt ttttaagacg 1400
 gattctcact ctgtggcca ggctggagt cagtgggtgc atctcagctc 1450
 actgcaaccc ccgcctcctg ggttcaagcg attctcctcc cccagcctcc 1500
 caagtagctg ggaggacagg tgtgagctgc cgcaccacgc ctgtttctct 1550
 ttttccactc ttcttttttc tcactcttt tctgggttgc ctgtcggtt 1600
 tcttatctgc ctgttttgca agcaccttct cctgtgtcct tgggagccct 1650
 gagacttctt tctctccttg cctccacca cctccaaagg tgctgagctc 1700
 acatccacac cccttgacg cgtccatgcc acagcccccc aaggggcccc 1750
 attgcaaaag catgcctgcc caccctcgt gtgccttagt cagtgtgtac 1800
 gtgtgtgtgt gtgtgtgtt ggggggtgg ggggtggtag ctggggattg 1850
 ggccctcttt ctcccagtg aggaaggtgt gcagtgtact tcccccttaa 1900

attaaaaaac atatatatat atatatttgg aggtcagtaa tttccaatgg 1950
 gcgggaggca ttaagcaccg accctgggtc cctaggcccc gcctggcact 2000
 cagccttgcc agagattggc tccagaattt ttgccaggct tacagaacac 2050
 ccaactgccta gaggccatct taaaggaagc aggggctgga tgcctttcat 2100
 cccaactatt ctctgtggta tgaaaaag 2128

<210> 31
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 31
 Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr
 1 5 10 15
 Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg
 20 25 30
 Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val
 35 40 45
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
 50 55 60
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
 80 85 90
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
 95 100 105
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
 110 115 120
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
 125 130 135
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
 140 145 150
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
 155 160 165
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
 170 175 180
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
 185 190 195
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
 200 205 210

Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu	215	220	225
Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu	230	235	240
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	245	250	255
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	260	265	270
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	275	280	285
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr	290	295	300
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala	305	310	315
His	Leu	Val	Phe	Val	Lys	Val									320		

<210> 32
 <211> 3680
 <212> DNA
 <213> Homo sapiens

<400> 32
 gaacgtgccca ccatgcccag ctaatttttg tatttttagt agagacgggg 50
 tttcaccatg ttggccaggc tggctttgaa ctcgtgacct catgatccgc 100
 tcacctcggc ctcccaaagt gctgggatta caggcatgag ccaactgacgc 150
 ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc 200
 taaacattgg gcaactacgt gaccaaaca gactgaattc cccaagagcc 250
 aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca 300
 ttattactca ctatgactaa gggtcacaaa tggggtagct tgatggagag 350
 tgatttggtta agagactaca gagggaggac agactaccaa gagggggggc 400
 aggaaagctc ctctgacgag gtggtatttc agcccaaact ggaagaatga 450
 gaaagagcta gccagccatc agaatagtcc agaagagatg gggagcacta 500
 cactcactac actttggcct gagaaaatag catgggattg gaggaggctg 550
 ggggaacacc actttgccg acctgggcag gaggcattga gggcttgaga 600
 aagggcaatg gcagtagcag tagaaaggac agggtaggag cagggacttt 650
 gcagggtgaa tcattaggtc ttatcaacag atatgggcaa gcaaagccag 700

gggagaattg atggtaatgc tgaggtttgg agccaggcta gatgggacag 750
 tgggtgggtga tgcaaaggaa agaggtcagg aagcagggcc agacgtgggg 800
 agaaggtgtg ggggttttgt ttccatcttg ccgagtctgc cggaatgtgg 850
 atgggaagac caagaggagg agcaaggggc agaggggaag ggaatcttaa 900
 agaagtcctg gatgccacac tcttcttctt tcctcctctt ccctctcctc 950
 agaggctca ctcgtggttc ttcatcttct gccctgcctc catctcctct 1000
 ggggtgctggg aaagtggagg attagctgaa gttttgcttc tcggggcctg 1050
 tctgaatctc cattgctttc tgggaggaca taattcacct gtcctagctt 1100
 cttatcatct tacatttccc tgtagccact gggacatatg tgggtgttct 1150
 tcctagctcc tgtctcctcc tcatgccttt gctgggtatg ggcatgttag 1200
 ggggaaggtc attgctgtca gaggggcact gactttctaa tgggtgttacc 1250
 caaggtgaat gttggagaca cagtcgcat gctgccaag tcccggcgag 1300
 ccctaactat ccaggagatc gctgcgctgg ccaggctcct cctgcatggt 1350
 atgcagcccc tcccatgttt ctggccactt tgcctttct cctcccgttt 1400
 gcacatccct ttggaactgt ttctgtgag tacatgctgg ggtctcccct 1450
 ttcttccctt gctcagggtga atctcagccc cttctccac ccaaagggtc 1500
 acatggatcc taactactgc cacccttcca cctccctgca cctgtgctcc 1550
 ctggcctggt cctttaccag gcttctccac cctccctat ctccagggtat 1600
 ttcccagggt gtgaaggacc acgtgaccaa gcctaccgcc atggcccagg 1650
 gccgagtggc tcacctcatt gagtgggaagg gctggagcaa gccgagtgac 1700
 tcacctgctg ccctggaatc agccttttcc tctattcag acctcagcga 1750
 gggcgaacaa gaggtcgtt ttgcagcagg agtggctgag cagtttgcca 1800
 tcgcggaagc caagctccga gcatggtctt cgggtggatg cgaggactcc 1850
 actgatgact cctatgatga ggactttgct gggggaatgg acacagacat 1900
 ggctgggcag ctgcccctgg ggccgcacct ccaggacctg ttcaccggcc 1950
 accggttctc ccggcctgtg cgccagggtt ccgtggagcc tgagagcgac 2000
 tgctcacaga ccgtgtcccc agacaccctg tgctctagtc tgtgcagcct 2050
 ggaggatggg ttgttgggt ccccggtggc gctggcctcc cagctgctgg 2100
 gcgatgagct gcttctcgcc aaactgcccc ccagccggga aagtgccttc 2150

cgcagcctgg gccactgga ggcccaggac tcactctaca actcgcccct 2200
 cacagagtcc tgcctttccc ccgcggagga ggagccagcc ccctgcaagg 2250
 actgccagcc actctgcca cactaacgg gcagctggga acggcagcgg 2300
 caagcctctg acctggcctc ttctgggggtg gtgtccttag atgaggatga 2350
 ggcagagcca gaggaacagt gaccacatc atgcctggca gtggcatgca 2400
 tccccgggt gctgccaggg gcagagcctc tgtgccaag tgtgggctca 2450
 aggctcccag cagagctcca cagcctagag ggctcctggg agcgtcgt 2500
 tctccgttgt gtgttttgca tgaaagtgt tggagaggag gcaggggctg 2550
 ggctgggggc gcatgtcctg ccccaactcc cggggcttgc cgggggttgc 2600
 ccggggcctc tggggcatgg ctacagctgt ggcagacagt gatgttcag 2650
 ttcttaaaat gccacacaca catttcctcc tcggataatg tgaaccacta 2700
 aggggggtgt gactgggctg tgtgagggtg ggggaggagg gggcccagca 2750
 acccccacc ctcccatgc ctctctctc tctgctttc ttctcactc 2800
 cgagtccatg tgcagtgtt gatagaatca ccccacctg gaggggctgg 2850
 ctctgccct ccgggagcct atgggttgag ccgtccctca agggcccctg 2900
 ccagctggg ctgtgtgtt gcttcattca cctctccatc gtctctaaat 2950
 cttctcttt ttctctaaag acagaaggtt tttgtctgt ttttctagtc 3000
 ggatcttctc ttctctggga ggctttgaa tgatgaaagc atgtaccctc 3050
 caccctttc ctggccccct aatggggcct gggcccttc ccaaccctc 3100
 ctaggatgtg cgggcagtgt gctggcgct cacagccagc cgggctgcc 3150
 attcacgag agctctctga gcgggaggtg gaagaaagga tggctctggt 3200
 tgccacagag ctgggacttc atgttcttct agagagggcc acaagagggc 3250
 cacaggggtg gccgggagtt gtcagctgat gcctgctgag aggcaggaat 3300
 tgtgccagt agtgacagtc atgaggaggt gtctcttctt ggggaggaaa 3350
 gaaggtagag ctttctgtc tgaatgaaag gccaaggcta cagtacaggg 3400
 ccccgccca gccagggtgt taatgccac gtagtgagg cctctggcag 3450
 atctgcatt ccaaggcac tggactgtac gtttttatg ttgtgggaag 3500
 ggtgggtggc tttagaatta agggccttgt aggctttggc aggtaagagg 3550
 gcccaaggta agaacgagag ccaacgggca caagcattct atatataagt 3600

gggtcattag gtgtttatatt tgttctatatt aagaatttgt tttattaaat 3650

taatataaaa atctttgtaa atctctaaaa 3680

<210> 33
<211> 335
<212> PRT
<213> Homo sapiens

<400> 33
Met Phe Leu Ala Thr Leu Ser Phe Leu Leu Pro Phe Ala His Pro
1 5 10 15
Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser
20 25 30
Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val
35 40 45
His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
50 55 60
Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
65 70 75
Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
80 85 90
Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
95 100 105
Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
110 115 120
Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
125 130 135
Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
140 145 150
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
155 160 165
Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
170 175 180
Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
185 190 195
His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
200 205 210
Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser
215 220 225
Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu
230 235 240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
305 310 315

Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
320 325 330

Glu Pro Glu Glu Gln
335

<210> 34
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct

<400> 34
tgtcctttgt ccagacttc tgtcc 25

<210> 35
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 35
ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcatgct 50

<210> 36
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 37
ggcgagccct aactatccag gag 23

<210> 38
<211> 39
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-39
<223> Synthetic construct.

<400> 38
ggagatcgct gcgctggcca ggtcctccct gcatggat 39

<210> 39
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 39
ctgctgcaaa gcgagcctct tg 22

<210> 40
<211> 2084
<212> DNA
<213> Homo sapiens

<400> 40
ggttcctggg cgctctgtta cacaagcaag atacagccag cccaccta 50
ttttgtttcc ctggcaccct cctgctcagt gcgacattgt cacacttaac 100
ccatctgttt tctctaagtc acgacagatt cctttcagac aggacaactg 150
tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200
tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250
caatctattc ttgccacatc aagggttgt tattccttta aaaaaaacc 300

aataccaaag aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350
caacgttggt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400
gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450
taaacctatt tctttgaaa gtgaagcaaa cttaaactca gataaagaaa 500
atataaccac ctcaaatctc aaggcgagtc attcccctcc tttgaatcta 550
cccaacaaca gccacggaat aacagatttc tccagtaact catcagcaga 600
gcattctttg ggcagtctaa aaccacatc taccatttcc acaagccctc 650
ccttgatcca tagctttgtt tctaaagtgc cttggaatgc acctatagca 700
gatgaagatc ttttgcccat ctgagacat cccaatgcta cacctgctct 750
gtcttcagaa aacttcactt ggtctttggt caatgacacc gtgaaaactc 800
ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850
ccatctgtga cccccttgat agtggaacca agtggtggc ttaccacaaa 900
cagtgatagc ttactgggt ttaccctta tcaagaaaaa acaactctac 950
agcctacctt aaaattcacc aataattcaa aactcttcc aaatacgtca 1000
gatcccaaaa aagaaaatag aaatacagga atagtattcg gggccatttt 1050
aggtgctatt ctgggtgtct cattgcttac tcttggtggc tacttgttgt 1100
gtgaaaaaag gaaaacggat tcattttccc atcggcgact ttatgacgac 1150
agaaatgaac cagttctgag attagacaat gcaccggaac cttatgatgt 1200
gagttttggg aattctagct actacaatcc aactttgaat gattcagcca 1250
tgccagaaag tgaagaaaat gcacgtgatg gcattcctat ggatgacata 1300
cctccacttc gtacttctgt atagaactaa cagcaaaag gcgttaaaca 1350
gcaagtgtca tctacatcct agccttttga caaattcatc tttcaaaagg 1400
ttacacaaaa ttactgtcac gtggattttg tcaaggagaa tcataaaagc 1450
aggagaccag tagcagaaat gtagacagga tgtatcatcc aaaggttttc 1500
tttcttacia ttttggccca tcctgaggca tttactaagt agccttaatt 1550
tgtattttag tagtattttc ttagtagaaa atatttggtg aatcagataa 1600
aactaaaaga tttcaccatt acagccctgc ctcataacta aataataaaa 1650
attattccac caaaaaattc taaaacaatg aagatgactc tttactgctc 1700
tgccctgaagc cctagtacca taattcaaga ttgcattttc ttaaatgaaa 1750

attgaaaggg tgctttttaaa agaaaatttg acttaaagct aaaaagagga 1800
catagcccag agtttctgtt attgggaaat tgaggcaata gaaatgacag 1850
acctgtattc tagtacgtta taattttcta gatcagcaca cacatgatca 1900
gccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950
aggaaagctg accctaccca ggaaagtaat agcttcttta aaagtcttca 2000
aagggttttg gaattttaac ttgtcttaat atatcttagg cttcaattat 2050
ttgggtgcct taaaaactca atgagaatca tggt 2084

<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
1 5 10 15
Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
20 25 30
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
110 115 120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330

Arg Thr Ser Val

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
 aacaggatct cctcttgcag tctgcagccc aggacgctga ttccagcagc 50
 gccttaccgc gcagcccgaa gattcactat ggtgaaaatc gccttcaata 100
 cccctaccgc cgtgcaaaag gaggaggcgc ggcaagaçgt ggaggccctc 150
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccaccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300
 tacaagtact tcatgcccac gagcaccatt taccgtggag agatgtgctt 350
 ttttgattct gaggatcctg caaattccct tcgtggagga gaggcctaact 400
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
 atcattgatg tgcctgtccc cagtttctct gatagtgacc ctgcagcaat 500
 tattcatgac tttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

ggaactgcta tctgatgccc ctcaatactt ctattgttat gcctccaaaa 600
 aatctggttag agctcttttg caaactggcg agtggcagat atctgcctca 650
 aacttatgtg gttcgagaag acctagtgtc tgtggaggaa attcgtgatg 700
 ttagtaacct tggcatcttt atttaccaac ttgcaataa cagaaagtcc 750
 ttccgccttc gtcgcagaga cctcttgctg ggtttcaaca aacgtgccat 800
 tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850
 ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900
 agaagtcaga gatttacaat atgacttta cattaagggt tatgggatac 950
 tcaagatatt tactcatgca ttactctat tgcttatgct ttaaaaaaag 1000
 gaaaaaaaaaaa aaactacta accactgcaa gctcttgtca aattttagtt 1050
 taattggcat tgcttgTTTT ttgaaactga aattacatga gtttcatttt 1100
 ttctttgcat ttataggggt tagatttctg aaagcagcat gaatatatca 1150
 cctaacatcc tgacaataaa ttccatccgt tgTTTTTTTT gtttgtttgt 1200
 tttttctttt cctttaagta agctctttat tcatcttatg gtggagcaat 1250
 tttaaaattt gaaatatatt aaattgtttt tgaacttttt gtgtaaaata 1300
 tatcagatct caacattgtt ggtttctttt gtttttcatt ttgtacaact 1350
 ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400
 ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450
 aatgcagtga ttcttttctca ctactatctg tattgtggaa tgcacaaaat 1500
 tgtgtaggtg ctgaatgctg taaggagttt aggttgatg aattctacaa 1550
 ccctataata aattttactc tatacaaaaa aaaaaaaa aa 1594

<210> 43
 <211> 263
 <212> PRT
 <213> Homo sapiens

<400> 43
 Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
 1 5 10 15
 Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
 20 25 30
 Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
 35 40 45
 Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50										55					60				
Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr					
				65					70					75					
Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys					
				80					85					90					
Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu					
				95					100					105					
Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp					
				110					115					120					
Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp					
				125					130					135					
Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr					
				140					145					150					
Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu					
				155					160					165					
Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe					
				170					175					180					
Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val					
				185					190					195					
Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn					
				200					205					210					
Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe					
				215					220					225					
Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala					
				230					235					240					
Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile					
				245					250					255					
Val	Glu	Thr	Lys	Ile	Cys	Gln	Glu												
				260															

<210> 44
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 44
 gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-20
 <223> Synthetic construct.

 <400> 45
 gggaactgct atctgatgcc 20

 <210> 46
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 46
 caggatctcc tcttgcatgc tgcagc 26

 <210> 47
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-28
 <223> Synthetic construct.

 <400> 47
 cttctcgaac cacataagtt tgaggcag 28

 <210> 48
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 48
 cacgattccc tccacagcaa ctggg 25

 <210> 49
 <211> 1969
 <212> DNA
 <213> Homo sapiens

 <400> 49
 ggaggaggga gggcgggcag ggcgcagccc agagcagccc cgggcaccag 50

cacggactct ctcttccagc ccaggtgccc cccactctcg ctccattcgg 100
cgggagcacc cagtcctgta cgccaaggaa ctggctcctgg gggcaccatg 150
gtttcggcgg cagccccag cctcctcatc cttctgttgc tgctgctggg 200
gtctgtgcct gctaccgacg cccgctctgt gcccctgaag gccacgttcc 250
tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggctcctcc 300
ccgagcctcc cgccaccctg gaccccgcc ctcagcccca catcgatggg 350
gccccagccc acaaccctgg ggggccatc acccccacc aacttcctgg 400
atgggatagt ggacttcttc cgccagtacg tgatgctgat tgctgtggtg 450
ggctccctgg cttttctgct gatgttcacg gtctgtgccg cggtcatcac 500
ccggcagaag cagaaggcct cggcctatta cccatcgtcc ttccccaaga 550
agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggcttcagt 600
gaggctcccc acagagcccc cgacagcagg cccgaggaag ccctggattc 650
ctcccggcag ctccaggccg acatcttggc cgccaccag aacctcaagt 700
ccccaccag ggctgcactg ggcggtgggg acggagccag gatggtggag 750
ggcaggggcg cagaggaaga ggagaagggc agccaggagg gggaccagga 800
agtccaggga catggggctc cagtggagac accagaggcg caggaggagc 850
cgtgctcagg ggtccttgag ggggctgtgg tggccgtga gggccaaggg 900
gagctggaag ggtctctctt gttagcccag gaagcccagg gaccagtggg 950
tcccccgaa agccctgtg cttgcagcag tgtccacccc agtgtctaac 1000
agtccctccg ggctgccagc cctgactgtc gggcccccaa gtggtcacct 1050
ccccgtgtat gaaaaggcct tcagccctga ctgcttcctg aactccctc 1100
cttggcctcc ctgtggtgcc aatcccagca tgtgctgatt ctacagcagg 1150
cagaaatgct ggtccccggg gccccggagg aatcttacca agtgccatca 1200
tccttcacct cagcagcccc aaagggtac atcctacagc acagctcccc 1250
tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300
ccccaaagt gctgggatta caggcgtgag ccaccgtgcc cgccccaaac 1350
tactttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400
aatactgctc ttaattttcc tgaaggtggc cccctgttcc tagttggctc 1450
aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctc 1500

caagcacccc cggcctgggg gtgagtttct catcccgcta ctgctgctgg 1550
 gatcaggttg aatgaatgga actcttcctg tctggcctcc aaagcagcct 1600
 agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtccga 1650
 ggggctgggg aagggtttct gacgcccagc ctggagcagg ggggccctgg 1700
 ccaccccctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750
 gtcagtcctc gacaggggagc ctgggctccg tcctgcttta gggaggctct 1800
 ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850
 gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900
 attccggcct gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1950
 aaaaaaaaa aaaaaaaga 1969

<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 50

Met	Val	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	Leu	
1				5					10					15	
Leu	Leu	Gly	Ser	Val	Pro	Ala	Thr	Asp	Ala	Arg	Ser	Val	Pro	Leu	
				20					25					30	
Lys	Ala	Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	
				35					40					45	
Gly	Ser	Ser	Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro	
				50					55					60	
Ala	Leu	Ser	Pro	Thr	Ser	Met	Gly	Pro	Gln	Pro	Thr	Thr	Leu	Gly	
				65					70					75	
Gly	Pro	Ser	Pro	Pro	Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe	
				80					85					90	
Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	
				95					100					105	
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	
				110					115					120	
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys	
				125					130					135	
Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe	
				140					145					150	
Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala	
				155					160					165	

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr
				170					175					180
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp
				185					190					195
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys
				200					205					210
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro
				215					220					225
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
				230					235					240
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly
				245					250					255
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro
				260					265					270
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val		
				275					280					

<210> 51
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
 gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca 50
 gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100
 gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150
 agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200
 cctggcctgc ctctgctgg ccctctgcct gggcagtggg gaggctggcc 250
 ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300
 ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350
 caaagaggcc ggaggggcag ctggctctaa agtcagttag gcccttggcc 400
 aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450
 ggcgagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500
 gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550
 acggagcaga tgctgtccgc ggctcctggc aggggggtgcc tggccacagt 600
 ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg 650
 ccttgagggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccggaac tcagcaggca gctttggaat gaatcctcag 750
 ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac 800
 caacactcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca 850
 gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900
 ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtg 950
 cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
 gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050
 agtggtgga gcagtggcaa cagtgggtggc agcagaggtg acagcggcag 1100
 tgagtctctc tggggatcca gcaccggctc ctctccggc aaccacggtg 1150
 ggagcggcgg aggaaatgga cataaaccg ggtgtgaaaa gccagggat 1200
 gaagcccgcg ggagcgggga atctgggatt cagggttca gaggacagg 1250
 agtttcagc aacatgagg aaataagcaa agagggaat cgcctccttg 1300
 gaggctctgg agacaattat cgggggcaag ggtcagctg gggcagtgga 1350
 ggaggtgacg ctgttggtg agtcaatact gtgaactctg agacgtctcc 1400
 tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
 gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500
 ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550
 ccctccttaa aacaccacc tctcatcact aatctcagcc cttgcccttg 1600
 aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52

<211> 440

<212> PRT

<213> Homo sapiens

<400> 52

Met	Lys	Phe	Gln	Gly	Pro	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Leu	Cys
1				5					10					15

Leu	Gly	Ser	Gly	Glu	Ala	Gly	Pro	Leu	Gln	Ser	Gly	Glu	Glu	Ser
			20						25					30

Thr	Gly	Thr	Asn	Ile	Gly	Glu	Ala	Leu	Gly	His	Gly	Leu	Gly	Asp
			35						40					45

Ala	Leu	Ser	Glu	Gly	Val	Gly	Lys	Ala	Ile	Gly	Lys	Glu	Ala	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50					55					60				
Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr
				65					70					75
Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly
				80					85					90
Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala
				95					100					105
Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val
				110					115					120
Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val
				125					130					135
Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile
				140					145					150
Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro
				155					160					165
Gly	Gly	Leu	Gly	Thr	Pro	Trp	Val	His	Gly	Tyr	Pro	Gly	Asn	Ser
				170					175					180
Ala	Gly	Ser	Phe	Gly	Met	Asn	Pro	Gln	Gly	Ala	Pro	Trp	Gly	Gln
				185					190					195
Gly	Gly	Asn	Gly	Gly	Pro	Pro	Asn	Phe	Gly	Thr	Asn	Thr	Gln	Gly
				200					205					210
Ala	Val	Ala	Gln	Pro	Gly	Tyr	Gly	Ser	Val	Arg	Ala	Ser	Asn	Gln
				215					220					225
Asn	Glu	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	Gly	Ser	Gly	Gly	Gly
				230					235					240
Ser	Ser	Asn	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gln	Ser	Gly	Ser	Ser
				245					250					255
Gly	Ser	Gly	Ser	Asn	Gly	Asp	Asn	Asn	Asn	Gly	Ser	Ser	Ser	Gly
				260					265					270
Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Gly	Ser
				275					280					285
Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser	Gly	Asn	Ser	Gly	Gly	Ser
				290					295					300
Arg	Gly	Asp	Ser	Gly	Ser	Glu	Ser	Ser	Trp	Gly	Ser	Ser	Thr	Gly
				305					310					315
Ser	Ser	Ser	Gly	Asn	His	Gly	Gly	Ser	Gly	Gly	Gly	Asn	Gly	His
				320					325					330
Lys	Pro	Gly	Cys	Glu	Lys	Pro	Gly	Asn	Glu	Ala	Arg	Gly	Ser	Gly
				335					340					345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn	350	355	360
Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser	365	370	375
Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly	380	385	390
Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser	395	400	405
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser	410	415	420
Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg	425	430	435
Ser Ser Arg Ile Pro	440		

<210> 53
 <211> 3580
 <212> DNA
 <213> Homo sapiens

<400> 53
 gaccggtccc tccggtcctg gatgtgcgga ctctgctgca gcgagggctg 50
 caggccccgcc gggcggtgct caccgtgccc tggctggtgg agtttctctc 100
 ctttgctgac catgttggtc ctttgctgga atattaccgg gacatcttca 150
 ctctcctgct gcgcctgcac cggagcttgg tgttgctgca ggagagttag 200
 gggaagatgt gtttcctgaa caagctgctg ctacttgctg tcctgggctg 250
 gcttttccag attcccacag tccctgagga cttgttcttt ctggaagagg 300
 gtccctcata tgcccttgag gtggacacag tagccccaga gcatggcttg 350
 gacaatgcgc ctgtggtgga ccagcagctg ctctacacct gctgccccta 400
 catcggagag ctccggaaac tgctcgcttc gtgggtgtca ggagtagtg 450
 gacggagtgg gggcttcattg aggaaaatca cccccaccac taccaccagc 500
 ctgggagccc agccttccca gaccagccag gggctgcagg cacagctcgc 550
 ccaggccttt ttccacaacc agccgccctc cttgcgccgg accgtagagt 600
 tcgtggcaga aagaattgga tcaaactgtg tcaaacatat caaggctaca 650
 ctggtggcag atctggtgcg ccaggcagag tcacttctcc aagagcagct 700
 ggtgacacag ggagaggaag ggggagaccc agcccagctg ttggagatct 750
 tgtgttccca gctgtgccct cacggggccc aggcattggc cctggggcgg 800

gagttctgtc aaaggaagag ccctggggct gtgcgggcgc tgcttccaga 850
ggagaccccc gcagccgttc tgagcagtgc agagaacatt gctgtggggc 900
ttgcaacaga gaaagcctgt gcttggtgtg cagccaacat cacagcactg 950
atcaggaggg aggtgaaagc agcagtgagt cgcacacttc gagcccagg 1000
tcctgaacct gctgcccggg gggagcggag gggctgctcc cgcgcctgac 1050
gtgctctcct tggccgtggg gccacgggac cctgacgagg gagtctcccc 1100
agagcatctg gaacagctcc taggccagct gggccagacg ctgcggtgcc 1150
gccagttcct gtgccacact gctgagcagc atctggcaaa gtgctctgtg 1200
gagttagctt ccctcctcgt tgcagatcaa attcctatcc tagggccccc 1250
ggcacagtac aggttgagga gagggcaggc tcgaaggctt ctgcacatgc 1300
tgctttcctt gtggaaggaa gactttcagg ggccggttcc gctgcagctg 1350
ctgctgagcc caagaaatgt ggggcttctg gcagacacaa ggccaaggga 1400
gtgggacttg ctgctattct tgctacggga gctggtggag aagggtctga 1450
tgggacggat ggagatagag gcctgcctgg gcagcctcca ccaggcccag 1500
tggccagggg actttgctga agaattagca aactgtcta atctgtttct 1550
agccgagccc cacctgccag aacccagct aagagcctgt gagttggtgc 1600
agccaaaccg gggcactgtg ctggcccaga gctagggctg agaagtggcc 1650
ctgccttggg cattgcacca gaaccctgga ccccgccctc acgaggaggc 1700
ccaagtgcc aatgcagacc ctactgggtt ggggtgtagc tgggtctaca 1750
gtcagacttc ctgctctaag ggtgtcactg cctggcatcc caccacgca 1800
atcctagagg aaggagagtt ggcctgattt gggattatgg cagaaaagtc 1850
cagagatgcc agtctggag tagaagaggt ggtgtttggt tatctcttgg 1900
atactaaatg aaatgagggt tgtgggcttg tcaacacaga attcaagcct 1950
catttgctat ccagcatct cttaaaactt tgtagtcttg gaattcatga 2000
cagaggcaaa tgactcctgc ttaacttatg aagaaagtta aaacatgaat 2050
cttgggagtc tacattttct tatcaccagg agctggactg ccatctcctt 2100
ataaatgcct aacacaggcc gggctctggtg gctcatgcct gtaatcccag 2150
cactttgaga ggcctgaggt cggcggactg cctgaggtca ggaattcaag 2200
accagcctgg ccaacatggc aaaaccccat ctctactaaa aataaaaaaa 2250

ttattagctg ggcatggtgg tgtgtgacctg taatcccagc tactcaggag 2300
 gatgaggcag gagacctgct tgaacctgga ggtggagggt gcagtgagcc 2350
 gaggtcgac cactgcactc cagtctgggt aacagagcga gactttctag 2400
 aaaaagccta acaaacagat aaggtaggac tcaaccaact gaaacctgac 2450
 tttccccctg taccttcagc ccctgtgcag gtagtaacct cttgagacct 2500
 ctccctgacc agggaccaag cacagggcat ttagagcttt ttagaataaa 2550
 ctggttttct ttaaaaaaaaa aaaaaaaaaa agggcgcccg cccttttttt 2600
 tttttttttt tttttttttt tttttttttt tttttttttt taaaaagggc 2650
 ttttattaaa attctcccca cacgatggct cctgcaatct gccacagctc 2700
 tggggcggtgt cctgtaggga aaggccctgt tttccctgag gcggggctgg 2750
 gcttgccat gggtcgcgg agctggccgt gcttgccgc ccggcgctgtg 2800
 tctagctgct tcttgccggg cacagagctg cggggtctgg gggcaccggg 2850
 agctaagagc aggcctctgt gcaggggtgg aggcctgtct cttaacgac 2900
 accctgaggt gtcctgaga tgctgggtcc accctgagtg gcacggggag 2950
 cagctgtggc cgggtgctct tcytaggcca gtccctggga aactaagctc 3000
 gggcccttct ttgcaaagac cgaggatggg gtgggtgtgg gggactcatg 3050
 gggaatggcc tgaggagcta cgtgtgaaga gggcgccggt ttgttgctg 3100
 cagcggcctg gagcgctct ctctgagcc tcagtttccc tttccgtcta 3150
 atgaagaaca tgccgtctcg gtgtctcagg gctattagga cttgccctca 3200
 ggaagtggcc ttggacgagc gtcattgtat tttcacaact gtcctgcgac 3250
 gttggcctgg gcacgtcatg gaatggccca tgtccctctg ctgcgtggac 3300
 gtcgcggtcg ggagtgcga gccagaggcg gggccagacg tgcgcctggg 3350
 ggtgagggga ggcgccccg gagggcctca caggaagttg ggctcccga 3400
 ccaccaggca gggcgggctc ccgccgccgc cgccgccacc accgtccagg 3450
 ggccggtaga caaagtggaa gtcgcgcttg ggctcgctgc gcagcaggta 3500
 gcccttgatg cagtgcggca gcgcgtcgtc cgccagctgg aagcagcgcc 3550
 cgtccaccag cacgaacagc cgggtgcgct 3580

<210> 54
 <211> 280
 <212> PRT
 <213> Homo sapiens

<400> 54

Met	Cys	Phe	Leu	Asn	Lys	Leu	Leu	Leu	Leu	Ala	Val	Leu	Gly	Trp
1				5					10					15
Leu	Phe	Gln	Ile	Pro	Thr	Val	Pro	Glu	Asp	Leu	Phe	Phe	Leu	Glu
				20					25					30
Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
				35					40					45
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
				50					55					60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
				80					85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
				95					100					105
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
				110					115					120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
				125					130					135
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
				140					145					150
Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu
				155					160					165
Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
				170					175					180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
				185					190					195
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg
				200					205					210
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala
				215					220					225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
				230					235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
				245					250					255
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
				260					265					270
Arg	Gly	Glu	Arg	Arg	Gly	Cys	Ser	Arg	Ala					
				275					280					

<210> 55
<211> 2401
<212> DNA
<213> Homo sapiens

<400> 55
tcccttgaca ggtctggtgg ctggttcggg gtctactgaa ggctgtcttg 50
atcaggaaac tgaagactct ctgcttttgc cacagcagtt cctgcagctt 100
ccttgaggtg tgaaccaca tcctgcccc cagggccacc tgcaggacgc 150
cgacacctac ccctcagcag acgccggaga gaaatgagta gcaacaaaga 200
gcagcgggtca gcagtgttcg tgatcctctt tgccctcatc accatcctca 250
tcctctacag ctccaacagt gccaatgagg tcttccatta cggctccctg 300
cggggccgta gccgccgacc tgtcaacctc aagaagtgga gcatcactga 350
cggctatgtc ccattctcg gcaacaagac actgccctct cggtgccacc 400
agtgtgtgat tgtcagcagc tccagccacc tgctgggcac caagctgggc 450
cctgagatcg agcgggctga gtgtacaatc cgcataatg atgcacccac 500
cactggctac tcagctgatg tgggcaacaa gaccacctac cgcgtcgtgg 550
cccattccag tgtgttccgc gtgctgagga ggccccagga gtttgtcaac 600
cggaccctcg aaaccgtgtt catcttctgg gggccccga gcaagatgca 650
gaagccccag ggcagcctcg tgcgtgtgat ccagcgagcg ggcttgtgt 700
tccccaatat ggaagcatat gccgtctctc ccggccgcat gcggcaattt 750
gacgacctct tccggggtga gacgggcaag gacagggaga agtctcattc 800
gtggttgagc acaggttgtt ttaccatggt gatcgcggtg gagttgtgtg 850
accacgtgca tgtctatggc atggtcccc ccaactactg cagccagcgg 900
ccccgcctcc agcgcatgcc ctaccactac tacgagccca aggggcccga 950
cgaatgtgtc acctacatcc agaatagagc cagtcgcaag ggcaaccacc 1000
accgcttcat caccgagaaa agggcttctt catcgtgggc ccagctgtat 1050
ggcatcacct tctccacccc ctctggacc taggccaccc agcctgtggg 1100
acctcaggag ggtcagagga gaagcagcct ccgccagcc gctaggccag 1150
ggaccatctt ctggccaatc aaggcttgct ggagtgtctc ccagccaatc 1200
agggccttga ggaggatgta tcctccagcc aatcagggcc tggggaatct 1250
gttggcgaat cagggatttg ggagtctatg tggtaatatca ggggtgtctt 1300

tcttgtgcag tcagggctctg cgcacagtca atcagggtag aggggggtatt 1350
tctgagtcaa tctgaggcta aggacatgtc ctttcccatg aggccttggt 1400
tcagagcccc aggaatggac cccccaatca ctccccactc tgctgggata 1450
atgggggtcct gtcccaagga gctgggaact tgggtgttgcc ccctcaattt 1500
ccagcaccag aaagagagat tgtgtggggg tagaagctgt ctggaggccc 1550
ggccagagaa tttgtggggg tgtggagggt gtgggggcg tgaggagggtc 1600
ccagaggtgg gaggctggca tccaggctct ggctctgccc tgagaccttg 1650
gacaaaccct tccccctctc tgggcaccct tctgccaca ccagtttcca 1700
gtgcggagtc tgagaccctt tccacctccc ctacaagtgc cctcgggtct 1750
gtcctccccg tctggaccct cccagccact atcccttgct ggaaggctca 1800
gctctttggg gggctctggg tgacctcccc acctcctgga aaactttagg 1850
gtatttttgc gcaaactcct tcagggttgg gggactctga aggaaacggg 1900
acaaaaccct aagctgtttt cttagccct cagccagctg ccattagctt 1950
ggctcttaaa gggccaggcc tccttttctg ccctctagca gggagggttt 2000
ccaactgttg gaggcgcctt tggggctgcc cctttgtctg gagtcaactg 2050
gggcttccga gggctcctc cgaccctctg tcgtcctggg atggctgtcg 2100
ggagctgtat cacctgggtt ctgtcccctg gctctgtatc aggcacttta 2150
ttaaagctgg gcctcagtgg ggtgtgtttg tctcctgctc ttctggagcc 2200
tggaaggaaa gggttcagg aggaggctgt gaggctggag ggaccagatg 2250
gaggaggcca gcagctagcc attgcacact ggggtgatgg gtgggggcg 2300
tgactgcccc agacttggtt ttgtaatgat ttgtacagga ataaacacac 2350
ctacgtccg gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 2400

a 2401

<210> 56

<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

Met	Ser	Ser	Asn	Lys	Glu	Gln	Arg	Ser	Ala	Val	Phe	Val	Ile	Leu
1				5					10					15

Phe	Ala	Leu	Ile	Thr	Ile	Leu	Ile	Leu	Tyr	Ser	Ser	Asn	Ser	Ala
				20					25					30

Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg		35	40	45
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro		50	55	60
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val		65	70	75
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro		80	85	90
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro		95	100	105
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg		110	115	120
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln		125	130	135
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly		140	145	150
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val		155	160	165
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala		170	175	180
Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly		185	190	195
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr		200	205	210
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val		215	220	225
His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro		230	235	240
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro		245	250	255
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly		260	265	270
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp		275	280	285
Ala	Gln	Leu	Tyr	Gly	Ile	Thr	Phe	Ser	His	Pro	Ser	Trp	Thr			290	295	

<210> 57

<211> 4277

<212> DNA

<213> Homo sapiens

<400> 57

gtttctcata gttggcgtct tctaaaggaa aaacactaaa atgaggaact 50
cagcggaccg ggagcgacgc agcttgaggg aagcatccct agctgttggc 100
gcagaggggc gaggtgaag ccgagtggcc cgaggtgtct gaggggctgg 150
ggcaaagggtg aaagagtttc agaacaagct tcctggaacc catgacccat 200
gaagtcttgt cgacatttat accgtctgag ggtagcagct cgaaactaga 250
agaagtggag tgttgccagg gacggcagta tctctttgtg tgaccctggc 300
ggcctatggg acgttggctt cagacctttg tgatacacca tgctgcgtgg 350
gacgatgacg gcgtggagag gaatgaggcc tgaggtcaca ctggcttgcc 400
tcctcctagc cacagcaggc tgctttgctg acttgaaacga ggtccctcag 450
gtcacctgcc agcctgcgtc caccgtccag aagcccggag gcactgtgat 500
cttgggctgc gtggtggaac ctccaaggat gaatgtaacc tggcgctga 550
atggaaagga gctgaatggc tcggatgatg ctctgggtgt cctcatcacc 600
cacgggaccc tcgtcatcac tgcccttaac aaccacactg tgggacggta 650
ccagtgtgtg gcccgatgc ctgcgggggc tgtggccagc gtgccagcca 700
ctgtgacact agccaatctc caggacttca agttagatgt gcagcacgtg 750
attgaagtgg atgagggaaa cacagcagtc attgcctgcc acctgcctga 800
gagccacccc aaagcccagg tccggtacag cgtcaaacia gagtggctgg 850
aggcctccag aggttaactac ctgatcatgc cctcaggga cctccagatt 900
gtgaatgcca gccaggagga cgaggcatg tacaagtgtg cagcctacia 950
cccagtgacc caggaagtga aaacctccgg ctccagcgac aggctacgtg 1000
tgcgcgcgtc caccgtgag gctgcccga tcactatccc cccagaggcc 1050
caaaccatca tcgtaccaa aggccagagt ctcatctgtg agtgtgtggc 1100
cagtggaatc ccacccccac gggtcacctg ggccaaggat gggctccagt 1150
tcaccggcta caacaagacg cgcttcctgc tgagcaacct cctcatcgac 1200
accaccagcg aggaggactc aggcacctac cgctgcatgg ccgacaatgg 1250
ggttgggcag cccggggcag cggtcacct ctacaatgtc caggtgtttg 1300
aaccctctga ggtcaccatg gagctatccc agctgggtcat cccctggggc 1350
cagagtgcca agcttacctg tgaggtgctg gggaaccccc cgcctccgt 1400
gctgtggctg aggaatgctg tgccctcat ctccagccag cgcctccggc 1450

tctcccgag gccctgcgc gtgctcagca tggggcctga ggacgaaggc 1500
gtctaccagt gcatggccga gaacgaggtt gggagcgccc atgccgtagt 1550
ccagctgcgg acctccaggc caagcataac cccaaggcta tggcaggatg 1600
ctgagctggc tactggcaca cctcctgtat caccctccaa actcggcaac 1650
cctgagcaga tgctgagggg gcaaccggcg ctccccagac ccccaacgtc 1700
agtggggcct gcttccccga agtgtccagg agagaagggg caggggggctc 1750
ccgccgaggc tccatcatc ctgagctcgc ccgcacctc caagacagac 1800
tcatatgaac tgggtgtggcg gcctcggcat gagggcagtg gccgggcgcc 1850
aatcctctac tatgtggtga aacaccgcaa gcaggtcaca aattcctctg 1900
acgattggac catctctggc attccagcca accagcaccg cctgaccctc 1950
accagacttg accccgggag cttgtatgaa gtggagatgg cagcttacia 2000
ctgtgcggga gagggccaga cagccatggt caccttccga actggacggc 2050
ggcccaaacc cgagatcatg gccagcaaag agcagcagat ccagagagac 2100
gaccctggag ccagtccccg gagcagcagc cagccagacc acggccgcct 2150
ctccccccca gaagctcccg acaggcccac catctccacg gcctccgaga 2200
cctcagtgtg cgtgacctgg attccccgtg ggaatgggtg gttcccaatc 2250
cagtccttcc gtgtggagta caagaagcta aagaaagtgg gagactggat 2300
tctggccacc agcgccatcc ccccatcgcg gctgtccgtg gagatcacgg 2350
gcctagagaa aggcacctcc tacaagtttc gagtccgggc tctgaacatg 2400
ctggggggaga gcgagcccag cgcacctctt cggccctacg tgggtgcggg 2450
ctacagcggg cgcgtgtacg agaggcccggt ggcaggtcct tatatcacct 2500
tcacggatgc ggtcaatgag accaccatca tgctcaagtg gatgtacatc 2550
ccagcaagta acaacaacac cccaatccat ggcttttata tctattatcg 2600
accacagac agtgacaatg atagtgacta caagaaggat atggtggaag 2650
gggacaagta ctggcactcc atcagccacc tgcagccaga gacctcctac 2700
gacattaaga tgagtgctt caatgaagga ggggagagcg agttcagcaa 2750
cgtgatgatc tgtgagacca aagctcgga gtcttctggc cagcctggct 2800
gactgccacc cccaactctg gccccaccac agccgccctt tcctgaaacc 2850
atagagcggc cgggtgggac tggggccatg gtggctcgct ccagcgacct 2900

gccctatctg attgtcgggg tcgtcctggg ctccatcggt ctcacatcgc 2950
 tcaccttcat ccccttctgc ttgtggaggg cctggtctaa gcaaaaacat 3000
 acaacagacc tgggttttcc tcgaagtgcc cttccaccct cctgcccgtc 3050
 tactatggtg ccattgggag gactcccagg ccaccaggcc agtggacagc 3100
 cctacctcag tggcatcagt ggacgggcct gtgctaattg gatccacatg 3150
 aataggggct gcccctcggc tgcagtgggc taccggggca tgaagcccca 3200
 gcagcactgc ccaggcgagc ttcagcagca gagtgacacc agcagcctgc 3250
 tgaggcagac ccattcttggc aatggatatg acccccaaag tcaccagatc 3300
 acgaggggct ccaagtctag cccggacgag ggctctttct tatacacact 3350
 gcccgacgac tccactcacc agctgctgca gcccacac gactgctgcc 3400
 aacgccagga gcagcctgct gctgtggggc agtcaggggt gaggagagcc 3450
 cccgacagtc ctgtcctgga agcagtgtgg gaccctccat ttcactcagg 3500
 gcccccatgc tgcttggggc ttgtgccagt tgaagaggtg gacagtcctg 3550
 actcctgcca agtgagtgga ggagactggt gtcccagca ccccgtaggg 3600
 gcctacgtag gacaggaacc tggaatgcag ctctccccgg ggccactggt 3650
 gcgtgtgtct ttgaaacac cacctctcac aatttaggca gaagctgata 3700
 tcccagaaag actatatatt gtttttttt taaaaaaaaa agaagaaaaa 3750
 agagacagag aaaattggta tttattttt tattatagcc atatttatat 3800
 atttatgcac ttgtaaataa atgtatatgt ttataattc tggagagaca 3850
 taaggagtcc taccggttga ggttgagag ggaaaataaa gaagctgcca 3900
 cctaacagga gtcaccagg aaagcaccgc acaggctggc gcgggacaga 3950
 ctccctaacct ggggcctctg cagtggcagg cgaggctgca ggaggccac 4000
 agataagctg gcaagaggaa ggatcccagg cacatggttc atcacgagca 4050
 tgagggaaca gcaaggggca cggtatcaca gcctggagac acccacacag 4100
 atggctggat ccggtgctac gggaaacatt ttcctaagat gcccatgaga 4150
 acagaccaag atgtgtacag cactatgagc attaaaaaac cttccagaat 4200
 caataatccg tggcaacata tctctgtaaa aacaaacact gtaacttcta 4250
 aataaatggt tagtcttccc tgtaaaa 4277

<210> 58
 <211> 1115

<212> PRT
 <213> Homo sapiens

<400> 58

Met	Leu	Arg	Gly	Thr	Met	Thr	Ala	Trp	Arg	Gly	Met	Arg	Pro	Glu	1	5	10	15
Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala	20	25	30	
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	35	40	45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	50	55	60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	65	70	75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	80	85	90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	95	100	105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	110	115	120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	125	130	135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	140	145	150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	155	160	165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	170	175	180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	185	190	195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	200	205	210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	215	220	225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	230	235	240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	245	250	255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	260	265	270	

Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu Leu	275	280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys Met	290	295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu Tyr	305	310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu Ser	320	325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys Glu	335	340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn Ala	350	355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg Ala	365	370	375
Leu Arg Val Leu	Ser Met Gly Pro Glu	Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu	Asn Glu Val Gly Ser	Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser	Arg Pro Ser Ile Thr	Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala	Thr Gly Thr Pro Pro	Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu	Gln Met Leu Arg Gly	Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser	Val Gly Pro Ala Ser	Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly	Ala Pro Ala Glu Ala	Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser	Lys Thr Asp Ser Tyr	Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly	Ser Gly Arg Ala Pro	Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys	Gln Val Thr Asn Ser	Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro	Ala Asn Gln His Arg	Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser	Leu Tyr Glu Val Glu	Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Glu Gly	Gln Thr Ala Met Val	Thr Phe Arg Thr Gly Arg			

560										565					570				
Arg	Pro	Lys	Pro	Glu	Ile	Met	Ala	Ser	Lys	Glu	Gln	Gln	Ile	Gln					
				575					580					585					
Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Ser	Gln	Pro	Asp				
				590					595					600					
His	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile					
				605					610					615					
Ser	Thr	Ala	Ser	Glu	Thr	Ser	Val	Tyr	Val	Thr	Trp	Ile	Pro	Arg					
				620					625					630					
Gly	Asn	Gly	Gly	Phe	Pro	Ile	Gln	Ser	Phe	Arg	Val	Glu	Tyr	Lys					
				635					640					645					
Lys	Leu	Lys	Lys	Val	Gly	Asp	Trp	Ile	Leu	Ala	Thr	Ser	Ala	Ile					
				650					655					660					
Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly					
				665					670					675					
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu					
				680					685					690					
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr					
				695					700					705					
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr					
				710					715					720					
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met					
				725					730					735					
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr					
				740					745					750					
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys					
				755					760					765					
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His					
				770					775					780					
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn					
				785					790					795					
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr					
				800					805					810					
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro					
				815					820					825					
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg					
				830					835					840					
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro					
				845					850					855					

Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	
				860					865					870	
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	
				875					880					885	
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	
				890					895					900	
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	
				905					910					915	
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	
				920					925					930	
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	
				935					940					945	
Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu	
				950					955					960	
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His	
				965					970					975	
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly	
				980					985					990	
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro	
				995					1000					1005	
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys	
				1010					1015					1020	
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg	
				1025					1030					1035	
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro	
				1040					1045					1050	
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu	
				1055					1060					1065	
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp	
				1070					1075					1080	
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly	
				1085					1090					1095	
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr	
				1100					1105					1110	
Pro	Pro	Leu	Thr	Ile											
				1115											

<210> 59

<211> 25

<212> DNA

<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 59
gggaaacaca gcagtcattg cctgc 25

<210> 60
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 60
gcacacgtag cctgtcgctg gaggc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-42
<223> Synthetic construct.

<400> 61
caccctaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
cgggaggctg ggtcgctcatg atccggaccc cattgtcggc ctctgcccatt 50
cgctgtctcc tcccaggctc ccgcggccga ccccgcgca acatgcagcc 100
cacgggccgc gaggggtccc gcgcgctcag ccggcggtat ctgcggcgctc 150
tgctgtctct gctactgtcg ctgctgtcgc ggcagcccgt aaccgcgcgcg 200
gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccag 250
cctcttcacc acgcccgggtg tccccagcgc cctcactacc ccaggcctca 300
ctacgccagg caccctaaag accctggacc ttcggggctc gcgcagggcc 350

ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400
 cctgagacag cggtacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
 tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500
 gccagttctt ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550
 cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600
 cctactctga actcgagctt gtgacctcag ctgaaggtct gaacagctct 650
 caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700
 cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750
 cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800
 agacaccaca tgtacaccaa cgtcagcggc ttgacaagct ttggtgagaa 850
 agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900
 catcgacac cttgataaga agggtcctgg aagtgtctca ggctcctgtg 950
 atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000
 tcccgatgat atcctgcagc ttctgaagaa cgggtggcatc gtgatgggtg 1050
 cactgtccat ggggggtgctg cagtgcaccc tgcttgctaa cgtgtccact 1100
 gtggcagatc actttgacca catcagggca gtcattggat ctgagttcat 1150
 cgggattggg ggaaattatg acgggactgg ccggttcctt caggggctgg 1200
 aggatgtgtc cacataccca gtcctgatag aggagttgct gagtcgtasc 1250
 tggagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300
 cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350
 tggaggctga gtttccatat gggcaactga gcacatccctg ccaactccac 1400
 ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450
 gccaaccaat cgggtcccct ggaggtcctc aaatgcctcc ccataccttg 1500
 ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550
 tgctgacaca gtcgggtccc gcagaggtca ctgtggcaaa gcctcacaaa 1600
 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
 cacatggaaa a 1661

<210> 63
 <211> 487
 <212> PRT
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	1	5	10	15
Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	20	25	30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	35	40	45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	50	55	60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	65	70	75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	80	85	90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	95	100	105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	110	115	120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	125	130	135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	140	145	150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	155	160	165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	170	175	180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	185	190	195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	200	205	210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	215	220	225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	230	235	240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	245	250	255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala				

260										265					270				
Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Glu	Val	Ser	Gln	Ala	Pro					
				275					280					285					
Val	Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu					
				290					295					300					
Leu	Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Asn	Gly	Gly					
				305					310					315					
Ile	Val	Met	Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu					
				320					325					330					
Leu	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Arg					
				335					340					345					
Ala	Val	Ile	Gly	Ser	Glu	Phe	Ile	Gly	Ile	Gly	Gly	Asn	Tyr	Asp					
				350					355					360					
Gly	Thr	Gly	Arg	Phe	Pro	Gln	Gly	Leu	Glu	Asp	Val	Ser	Thr	Tyr					
				365					370					375					
Pro	Val	Leu	Ile	Glu	Glu	Leu	Leu	Ser	Arg	Xaa	Trp	Ser	Glu	Glu					
				380					385					390					
Glu	Leu	Gln	Gly	Val	Leu	Arg	Gly	Asn	Leu	Leu	Arg	Val	Phe	Arg					
				395					400					405					
Gln	Val	Glu	Lys	Val	Arg	Glu	Glu	Ser	Arg	Ala	Gln	Ser	Pro	Val					
				410					415					420					
Glu	Ala	Glu	Phe	Pro	Tyr	Gly	Gln	Leu	Ser	Thr	Ser	Cys	His	Ser					
				425					430					435					
His	Leu	Val	Pro	Gln	Asn	Gly	His	Gln	Ala	Thr	His	Leu	Glu	Val					
				440					445					450					
Thr	Lys	Gln	Pro	Thr	Asn	Arg	Val	Pro	Trp	Arg	Ser	Ser	Asn	Ala					
				455					460					465					
Ser	Pro	Tyr	Leu	Val	Pro	Gly	Leu	Val	Ala	Ala	Ala	Thr	Ile	Pro					
				470					475					480					
Thr	Phe	Thr	Gln	Trp	Leu	Cys													
				485															

<210> 64
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 65
gtcacacaca gctctggcag ctgag 25

<210> 66
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 66
ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67
<211> 1564
<212> DNA
<213> Homo sapiens

<400> 67
tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50
aacaccaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100
ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
gcccattgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400
atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450
gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcggaag acagtcttcg 650
 atcggcacia gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700
 ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750
 ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800
 ctcttctcc ctaactttag aaatgttgta cttggctatt ttgattaggg 850
 aagagggatg tgggtctctga tctctgttgt cttcttgggt ctttggggtt 900
 gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950
 ctcaggagtg gatgcgatct gtctctctg gctccactct tgccgccttc 1000
 cagctctgag tcttgggaat gttgttacct ttggaagata aagctgggtc 1050
 ttcaggaact cagtgtcttg gaggaagca tggcccagca ttcagcatgt 1100
 gttcctttct gcagtgggtc ttatcaccac ctccctccca gccccggcgc 1150
 ctcagcccca gcccagctc cagccctgag gacagctctg atgggagagc 1200
 tgggccccct gagcccactg ggtcttcagg gtgcactgga agctgggtgt 1250
 cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata 1300
 ctctgtgcc ggtcccctca cctgcacttg aggggtcttg gcagtccctc 1350
 ctctccccag tgtccacagt cactgagcca gacggtcggg ttggaacatga 1400
 gactcgaggc tgagcgtgga tctgaacacc acagcccctg tacttgggtt 1450
 gcctcttgtc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500
 tcctcttgtc ttagagttgt gtgtaaatca aggaagccat cattaaattg 1550
 ttttatttct ctca 1564

<210> 68
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
 1 5 10 15
 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
 20 25 30
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu	
				65					70					75	
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val	
				80					85					90	
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr	
				95					100					105	
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp	
				110					115					120	
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala	
				125					130					135	
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	
				140					145					150	
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys	
				155					160					165	
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys	
				170					175					180	

Met Leu Ser

<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
 agcgggtctc gcttggttc cgctaatttc tgtcctgagg cgtgagactg 50
 agttcatagg gtctgggtc cccgaaccag gaagggttga gggaacacaa 100
 tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggtcctccc 150
 tccctttgca ttcccacccc tccgggcttt gcgtcttcct ggggaccccc 200
 tcgccgggag atggccggtg tgatgcggag caaggattcg tcctgctgcc 250
 tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300
 tcgcgggcc aactcaactc catcaagtcc tctctgggcg gggagacgcc 350
 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400
 gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500
 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgtgc caccgagatg 550
 gcatgtgtc cccagtagc cgctgcaata atggcatctg tatccagtt 600
 actgaaagca tottaacccc tcacatccc gctctggatg gtactcggca 650

cagagatcga aaccacgggtc attactcaaa ccatgacttg ggatggcaga 700
atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750
gacccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg 800
tcatttctgg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850
gtaccaaaaca acgcaagaag ggttctcatg ggctggaaat tttccagcgt 900
tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950
ctcttccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000
ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050
catggtggaa aataaggttc agatgcagaa gaatggctaa aataagaaac 1100
gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150
aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200
caacttgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250
agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300
aagagtttag gttgtgctgg aggagagggt tccttcagat tgctgattgc 1350
ttatacaaat aacctacatg ccagatttct attcaacgtt agagtttaac 1400
aaaatactcc tagaataact tgttatacaa taggttctaa aaataaaatt 1450
gctaaacaag aatgaaaac atggagcatt gttaatttac aacagaaaat 1500
taccttttga tttgtaacac tacttctgct gttcaatcaa gagtcttggt 1550
agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600
cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650
ccacaaatac ttttttttca aaattttagt ttacctgta attaataaga 1700
actgatacaa gacaaaaaca gttccttcag attctacgga atgacagtat 1750
atctctcttt atcctatgtg attcctgctc tgaatgcatt atattttcca 1800
aactataccc ataaattgtg actagtaaaa tacttacaca gagcagaatt 1850
ttcacagatg gcaaaaaaat ttaaagatgt ccaatatatg tgggaaaaga 1900
gctaacagag agatcattat ttcttaaaga ttggccataa cctatatattt 1950
gatagaatta gattggtaaa tacatgtatt catacact ctgtggtaat 2000
agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050
aaaacttttt cgtttgttca ggttttggca acacatagat catatgtctg 2100

aggcacaagt tggctgttca tctttgaaac caggggatgc acagtctaaa 2150
 tgaatatctg catgggattt gctatcataa tatttactat gcagatgaat 2200
 tcagtgtgag gtcctgtgtc cgtactatcc tcaaattatt tattttatag 2250
 tgctgagatc ctcaaataat ctcaatttca ggagggttca caaaatgtac 2300
 tcctgaagta gacagagtag tgagggttca ttgccctcta taagcttctg 2350
 actagccaat ggcacatcc aattttcttc ccaaacctct gcagcatctg 2400
 ctttattgcc aaagggttag tttcggtttt ctgcagccat tgcgggttaa 2450
 aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500
 accacagttt cttaaattctt tgaaaccact ttactacttt ttttaaactt 2550
 aactcagttc taaatacttt gtctggagca caaaacaata aaagggttatc 2600
 ttatagtcgt gactttaaac tttgttagac cacaattcac tttttagttt 2650
 tcttttactt aaatcccatc tgcagtctca aatttaagtt ctcccagtag 2700
 agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750
 tatttactaa gatgattaag acttacattt tctgcacagg tctgcaaaaa 2800
 caaaaattat aaactagtcc atccaagaac caaagtttgt ataaacaggt 2850
 tgctataagc ttgtgaaatg aaaatggaac atttcaatca aacatttcct 2900
 atataacaat tattatattt acaatttggg ttctgcaata tttttcttat 2950
 gtccaccctt ttaaaaatta ttatttgaag taatttattt acaggaaatg 3000
 ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050
 gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100
 taagataaaa tctattaaat ttttctcttc taaaaactga aaaaaaaaaa 3150
 aaaaaaaaaa aaaaaaaaaa 3170

<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

Met	Ala	Ala	Leu	Met	Arg	Ser	Lys	Asp	Ser	Ser	Cys	Cys	Leu	Leu
1				5					10				15	

Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25					30

Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40					45

Thr	Pro	Gly	Gln	Ala	Ala	Asn	Arg	Ser	Ala	Gly	Met	Tyr	Gln	Gly	
				50					55					60	
Leu	Ala	Phe	Gly	Gly	Ser	Lys	Lys	Gly	Lys	Asn	Leu	Gly	Gln	Ala	
				65					70					75	
Tyr	Pro	Cys	Ser	Ser	Asp	Lys	Glu	Cys	Glu	Val	Gly	Arg	Tyr	Cys	
				80					85					90	
His	Ser	Pro	His	Gln	Gly	Ser	Ser	Ala	Cys	Met	Val	Cys	Arg	Arg	
				95					100					105	
Lys	Lys	Lys	Arg	Cys	His	Arg	Asp	Gly	Met	Cys	Cys	Pro	Ser	Thr	
				110					115					120	
Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu	
				125					130					135	
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg	
				140					145					150	
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu	
				155					160					165	
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly	
				170					175					180	
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys	
				185					190					195	
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln	
				200					205					210	
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu	
				215					220					225	
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys	
				230					235					240	
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val	
				245					250					255	

Cys Gln Lys Ile

<210> 71
 <211> 1809
 <212> DNA
 <213> Homo sapiens

<400> 71
 tctcaatctg ctgacctcgt gatccgcctg accttgtaat ccacctacct 50
 tggcctccca aagtgttggg attacaggcg tgagccaccg cgcccgccca 100
 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatatt catgtagtat tttctaagtt 250
atatttttagt aattcatatg ttttagatta taggttttaa catacttgtg 300
aaaataacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350
ggatttgttc ttttatcccc cttttaaagt catccgtcct tggctcagga 400
tttggagagc ttgcaccacc aaaaatggca aacatcacca gtcgccagat 450
tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500
gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550
ctcaagcccc caacatccca gtccctcagtc ctcaagtcac ttgacttcaa 600
atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650
agcaccagag ccaggcagtc actgttcctc ctccctggtt ggagtccttt 700
ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750
tgtgaacaag cttttgcagc ttcccagcac gaccattgaa aatatctctg 800
tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850
atacccccag cttctaagat ccagcttct gcagtggaaa tgcctggttc 900
agcagatgtc acaggattaa atgtgcagtt tggggctctg gaatttgggt 950
cagaaccttc tctctctgaa tttggatcag ctccaagcag tgaaaatagt 1000
aatcagattc ccatcagctt gtattcgaag tctttaagtg agcctttgaa 1050
tacatcttta tcaatgacca gtgcagtaca gaactccaca tatacaactt 1100
ccgtcattac ctccctcagc ctgacaagct catcactgaa ttctgctagt 1150
ccagtagcaa tgtcttcctc ttatgaccag agttctgtgc ataacaggat 1200
cccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250
tgaatggaca tgggtggtgg cgaagtcagc agacactaga cagtaagtat 1300
agcagcaagc tactcttgtc atggctggtg ccaaccaaag agaggaagag 1350
gatagctcac gtgatgtgga aaacaccagt tggatcaatgg ctcatctggt 1400
aaaaagcagc ccttttgctt ttttgttttt ggaccaggtg ttggctgtgg 1450
tggtattaga aatgtcttaa ccacagcaag aaggaggtgg tggctctata 1500
ttcttctgcc ctaatcagac tgcaccacaa gtgcagcata cagtatgcat 1550
tttaaagatg cttgggccag gcgggggtgg tgatgcccac aatcccagtg 1600
ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700
gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750
gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800
ctgaaaaga 1809

<210> 72
<211> 363
<212> PRT
<213> Homo sapiens

<400> 72
Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile
1 5 10 15
Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly
20 25 30
Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
35 40 45
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
50 55 60
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
65 70 75
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
80 85 90
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
95 100 105
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
110 115 120
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
125 130 135
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
140 145 150
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
155 160 165
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
170 175 180
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
185 190 195
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
200 205 210
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
215 220 225

Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275					280					285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290					295					300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305					310					315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320					325					330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335					340					345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
				350					355					360

Leu Ile Arg

<210> 73

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-26

<223> Synthetic construct.

<400> 73

aattcatggc aaatatttcc cttccc 26

<210> 74

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 74

tggtaaactg gcccaaactc gg 22

<210> 75

<211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcac cgcgccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
gccgagtggg acaaagcctg gggctgggcg ggggccatgg cgctgccatc 50
ccgaatcctg ctttgaaaac ttgtgcttct gcagagctct gctgttctcc 100
tgcaactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggaggt 200
caccgacggc cccccggcca cccccgccta ctgggacggc gagaaggagg 250
tgctggcggt ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300
gggcacgtgt ggaccgaccg gcacgtggag gaggtcaac aggtgggtgca 350
ctgggaccgg cagccgcccc gggccccgca cgaccgcgcg gaccgcctgc 400
tggacctcta cgcgtcgggc gagcgccgcg cctacgggcc cttttttctg 450
cgcgaccgcg tggctgtggg cgcggtatgcc tttagcgcg gtgacttctc 500
actgcgtatc gagccgctgg aggtcgccga cgagggcacc tactcctgcc 550
acctgcacca ccattactgt ggcctgcacg aacgccgcgt ctccacctg 600
acggtcgccc aacccacgc ggagccgcc ccccggggt ctccgggcaa 650
cggctccagc cacagcggcg cccagggccc agacccaca ctggcgcgcg 700
gccacaacgt catcaatgtc atcgtccccg agagccgagc ccacttcttc 750
cagcagctgg gctacgtgct ggccacgctg ctgctcttca tctgctact 800
ggtcactgtc ctctggccg cccgcaggcg ccgcggaggc tacgaatact 850
cggaccagaa gtcgggaaag tcaaagggga aggatgttaa cttggcgag 900
ttcgctgtgg ctgcagggga ccagatgctt tacaggagtg aggacatcca 950
gctagattac aaaaacaaca tctgaagga gagggcgag ctggcccaca 1000
gccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050

aactgcaaat agggaggccc tgggctcctg gctgggccag cagctgcacc 1100
tctcctgtct gtgctcctcg gggcatctcc tgatgctccg gggctcacc 1150
cccttcacagc ggctggtccc gctttcctgg aatttggcct gggcgtatgc 1200
agaggccgcc tccacacccc tccccagg gcttggtggc agcatagccc 1250
ccacccctgc ggcctttgct cacgggtggc cctgccacc cctggcacia 1300
ccaaaatccc actgatgcc atcatgccct cagacccttc tgggctctgc 1350
ccgctggggg cctgaagaca ttcctggagg aactcccat cagaacctgg 1400
cagccccaaa actggggtca gcctcagggc aggagtccca ctctccagg 1450
gctctgctcg tccggggctg ggagatgttc ctggaggagg aactcccat 1500
cagaacttgg cagccttgaa gttgggtgca gcctcggcag gactccact 1550
cctcctgggg tgctgcctgc caccaagagc tccccacct gtaccaccat 1600
gtgggactcc aggcaccatc tgttctcccc agggacctgc tgacttgaat 1650
gccagccctt gctcctctgt gttgctttgg gccacctggg gctgcacccc 1700
ctgcccttct tctgccccat ccctacccta gccttgctct cagccacctt 1750
gatagtcact gggctccctg tgacttctga ccctgacacc cctcccttgg 1800
actctgcctg ggctggagtc tagggctggg gctacatttg gcttctgtac 1850
tggtgagga caggggaggg agtgaagttg gtttgggtg gcctgtgttg 1900
ccactctcag caccacacat ttgcatctgc tgggtggacct gccaccatca 1950
caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

Met	Ala	Leu	Pro	Ser	Arg	Ile	Leu	Leu	Trp	Lys	Leu	Val	Leu	Leu
1				5					10					15
Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp
				20					25					30
Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu
				35					40					45
Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro
				50					55					60
Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val
				65					70					75

Ala Arg Gly Ala	Pro	Ala	Leu	Leu	Thr	Cys	Val	Asn	Arg	Gly	His
	80					85					90
Val Trp Thr Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His
	95					100					105
Trp Asp Arg Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg
	110					115					120
Leu Leu Asp Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro
	125					130					135
Leu Phe Leu Arg	Asp	Arg	Val	Ala	Val	Gly	Ala	Asp	Ala	Phe	Glu
	140					145					150
Arg Gly Asp Phe	Ser	Leu	Arg	Ile	Glu	Pro	Leu	Glu	Val	Ala	Asp
	155					160					165
Glu Gly Thr Tyr	Ser	Cys	His	Leu	His	His	His	Tyr	Cys	Gly	Leu
	170					175					180
His Glu Arg Arg	Val	Phe	His	Leu	Thr	Val	Ala	Glu	Pro	His	Ala
	185					190					195
Glu Pro Pro Pro	Arg	Gly	Ser	Pro	Gly	Asn	Gly	Ser	Ser	His	Ser
	200					205					210
Gly Ala Pro Gly	Pro	Asp	Pro	Thr	Leu	Ala	Arg	Gly	His	Asn	Val
	215					220					225
Ile Asn Val Ile	Val	Pro	Glu	Ser	Arg	Ala	His	Phe	Phe	Gln	Gln
	230					235					240
Leu Gly Tyr Val	Leu	Ala	Thr	Leu	Leu	Leu	Phe	Ile	Leu	Leu	Leu
	245					250					255
Val Thr Val Leu	Leu	Ala	Ala	Arg	Arg	Arg	Arg	Gly	Gly	Tyr	Glu
	260					265					270
Tyr Ser Asp Gln	Lys	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Asp	Val	Asn
	275					280					285
Leu Ala Glu Phe	Ala	Val	Ala	Ala	Gly	Asp	Gln	Met	Leu	Tyr	Arg
	290					295					300
Ser Glu Asp Ile	Gln	Leu	Asp	Tyr	Lys	Asn	Asn	Ile	Leu	Lys	Glu
	305					310					315
Arg Ala Glu Leu	Ala	His	Ser	Pro	Leu	Pro	Ala	Lys	Tyr	Ile	Asp
	320					325					330
Leu Asp Lys Gly	Phe	Arg	Lys	Glu	Asn	Cys	Lys				
	335					340					

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<400> 78

cgccggaggc agcggcggcg tggcgacgcg gcgacatggc cgttgtctca 50
gaggacgact ttcagcacag ttcaaactcc acctacggaa ccacaagcag 100
cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150
cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200
atcttcttca gcctgggcat tggcagtcta ctgccatgga acttctttat 250
cactgccaag gagtactgga tgttcaaact cgcgaactcc tccagcccag 300
ccaccgggga ggaccctgag ggctcagaca tcctgaacta ctttgagagc 350
taccttgccg ttgcctccac cgtgccctcc atgctgtgcc tgggtggcaa 400
cttctgtctt gtcaacaggg ttgcagtcca catccgtgtc ctggcctcac 450
tgacgggcat cctggccatc ttcatggtga taactgcact ggtgaagggtg 500
gacacttctt cctggaccgc tgggtttttt gcggtcacca ttgtctgcat 550
ggtgatcttc agcgggtgcct ccactgtctt cagcagcagc atctacggca 600
tgaccggctc ctttctatg aggaactccc aagcactgat atcaggagga 650
gccatgggcg ggacggtcag cgccgtggcc tcattggtgg acttggctgc 700
atccagtgat gtgaggaaca gcgcctggc cttcttctg acggccacca 750
tcttctctgt gctctgcatg ggactctacc tgctgctgtc caggctggag 800
tatgccaggt actacatgag gcctgttctt gcggcccatg tgtttcttg 850
tgaagaggag cttccccagg actccctcag tgcccttcg gtggcctcca 900
gattcattga ttccacaca cccctctcc gcccctcct gaagaagacg 950
gccagcctgg gcttctgtgt cacctacgtc ttcttcatca ccagcctcat 1000
ctaccccgcc gtctgcacca acatcgagtc cctcaacaag ggctcgggct 1050
cactgtggac caccaagttt ttcaccccc tcactacctt cctcctgtac 1100
aactttgctg acctatgtgg ccggcagtc accgcctgga tccagggtgc 1150
agggcccaac agcaaggcgc tcccagggtt cgtgctcctc cggacctgcc 1200
tcacccccct cttcgtgtc tgtaactacc agccccgct ccacctgaag 1250
actgtggtct tccagtccga tgtgtacccc gcactcctca gctccctgct 1300
ggggctcagc aacggctacc tcagcacctt ggcctcctc tacgggccta 1350
agattgtgcc caggagctg gctgaggcca cgggagtggg gatgtccttt 1400
tatgtgtgct tgggcttaac actgggctca gcctgctcta cctcctggt 1450

gcacctcatc tagaaggag gacacaagga cattggtgct tcagagcctt 1500
tgaagatgag aagagagtgc aggagggctg ggggccatgg aggaaaggcc 1550
taaagtttca cttggggaca gagagcagag cacactcggg cctcatccct 1600
cccaagatgc cagttagcca cgtccatgcc cattccgtgc aaggcagata 1650
ttccagtcat attaacagaa cactcctgag acagttgaag aagaaatagc 1700
acaaatcagg ggtactccct tcacagctga tggttaacat tccaccttct 1750
ttctagccct tcaaagatgc tgccagtgtt cgccctagag ttattacaaa 1800
gccagtgcc aaaccagcc atgggctctt tgcaacctcc cagctgcgct 1850
cattccagct gacagcgaga tgcaagcaaa tgctcagctc tccttaccct 1900
gaaggggtct ccctggaatg gaagtcacct ggcatggtca gtcctcaggc 1950
ccaagactca agtgtgcaca gaccctgtg ttctgcgggt gaacaactgc 2000
ccactaacca gactggaaaa ccagaaaga tgggccttcc atgaatgctt 2050
cattccagag ggaccagagg gcctccctgt gcaagggatc aagcatgtct 2100
ggcctgggtt ttcaaaaaa gagggatcct catgacctgg tggcttatgg 2150
cctgggtcaa gatgagggtc ttccagtgtt cctgtttaca acatgtcaaa 2200
gccattgggt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser	1	5	10	15
Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala	20	25	30	
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg	35	40	45	
Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu	50	55	60	
Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys	65	70	75	
Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr	80	85	90	
Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser	95	100	105	

Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys			

	395	400	405
Thr Val Val Phe	Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser	Ser
	410	415	420
Leu Leu Gly Leu	Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu	Leu
	425	430	435
Tyr Gly Pro Lys	Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr	Gly
	440	445	450
Val Val Met Ser	Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly	Ser
	455	460	465
Ala Cys Ser Thr	Leu Leu Val His Leu	Ile	
	470	475	

<210> 80
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 80
 ttttgcggtc accattgtct gc 22

<210> 81
 <211> 23
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Artificial sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 81
 cgtaggtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 82
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83
 <211> 1844

<212> DNA
<213> Homo sapiens

<400> 83

gacagtggag ggcagtggag aggaccgcgc tgtcctgctg tcaccaagag 50
ctggagacac catctccac cgagagtcac ggccccattg gccctgcacc 100
tcctcgctct cgtccccatc ctctcagcc tggcggcctc ccaggactgg 150
aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200
ctatgagcag ctgctcaagg tggcgacctg ggggctcaat cggaccctga 250
agccccagag ggtgattgtg gttggcgctg gtgtggccgg gctggtggcc 300
gccaaggtgc tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350
taacaggatc gggggccgca tcttcaccta ccgggaccag aacacgggct 400
ggattgggga gctgggagcc atgcgcatgc ccagctctca caggatcctc 450
cacaagctct gccagggcct ggggctcaac ctgaccaagt tcaccagta 500
cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550
tggcggagaa ggtgcccag aagctgggct acgccttgcg tccccaggaa 600
aaggggcact cgcccgaaga catctaccag atggctctca accaggccct 650
caaagacctc aaggcactgg gctgcagaaa ggcgatgaag aagtttgaaa 700
ggcacacgct cttggaatat cttctcgagg aggggaacct gagccggccg 750
gccgtgcagc ttctgggaga cgtgatgtcc gaggatggct tcttctatct 800
cagcttcgcc gagggccctc gggccacag ctgcctcagc gacagactcc 850
agtacagccg catcgtgggt ggctgggacc tgctgccgcg cgcgctgctg 900
agctcgtgt cggggcttgt gctgttgaa gcgcccgtgg tggcgatgac 950
ccagggaccg cacgatgtgc acgtgcagat cgagacctct cccccggcgc 1000
ggaatctgaa ggtgctgaag gccgacgtgg tgctgctgac ggcgagcgga 1050
ccggcggtga agcgcatcac cttctcgccg ccgctgcccc gccacatgca 1100
ggaggcgctg cggaggctgc actacgtgcc ggccaccaag gtgttcctaa 1150
gcttcgcag gcccttctgg cgcgaggagc acattgaagg cggccactca 1200
aacaccgatc gcccgctcgc catgattttc taccgcccgc cgcgagagg 1250
cgcgctgctg ctggcctcgt acacgtggc ggacgcggcg gcagcgttcg 1300
ccggcttgag ccgggaagag gcgttgcgct tggcgctcga cgacgtggcg 1350

gcattgcacg ggcctgtcgt gcgccagctc tgggacggca ccggcgtcgt 1400
 caagcggttg gcgaggacc agcacagcca ggggtggcttt gtggtacagc 1450
 cgccggcgct ctggcaaacc gaaaaggatg actggacggg cccttatggc 1500
 cgcactact ttgccggcga gcacaccgcc taccgcacg gctgggtgga 1550
 gacggcggtc aagtcggcgc tgcgcgccgc catcaagatc aacagccgga 1600
 aggggcctgc atcgacacg gccagccccg aggggcacgc atctgacatg 1650
 gaggggcagg ggcattgtca tggggtggcc agcagcccct cgcattgacct 1700
 ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750
 aaaacacgac ccacacgagg acctcgcatt aaagtatttt cggaaaaaaaa 1800
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 84
 Met Ala Pro Leu Ala Leu His Leu Leu Val Leu Val Pro Ile Leu
 1 5 10 15
 Leu Ser Leu Val Ala Ser Gln Asp Trp Lys Ala Glu Arg Ser Gln
 20 25 30
 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
 35 40 45
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
 50 55 60
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
 80 85 90
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
 95 100 105
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
 110 115 120
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
 125 130 135
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
 140 145 150
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
 155 160 165

Leu Gly Tyr Ala	Leu Arg Pro Gln Glu	Lys Gly His Ser Pro	Glu
170	175	180	
Asp Ile Tyr Gln	Met Ala Leu Asn Gln	Ala Leu Lys Asp Leu	Lys
185	190	195	
Ala Leu Gly Cys	Arg Lys Ala Met Lys	Lys Phe Glu Arg His	Thr
200	205	210	
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly	Asn Leu Ser Arg Pro	Ala
215	220	225	
Val Gln Leu Leu	Gly Asp Val Met Ser	Glu Asp Gly Phe Phe	Tyr
230	235	240	
Leu Ser Phe Ala	Glu Ala Leu Arg Ala	His Ser Cys Leu Ser	Asp
245	250	255	
Arg Leu Gln Tyr	Ser Arg Ile Val Gly	Gly Trp Asp Leu Leu	Pro
260	265	270	
Arg Ala Leu Leu	Ser Ser Leu Ser Gly	Leu Val Leu Leu Asn	Ala
275	280	285	
Pro Val Val Ala	Met Thr Gln Gly Pro	His Asp Val His Val	Gln
290	295	300	
Ile Glu Thr Ser	Pro Pro Ala Arg Asn	Leu Lys Val Leu Lys	Ala
305	310	315	
Asp Val Val Leu	Leu Thr Ala Ser Gly	Pro Ala Val Lys Arg	Ile
320	325	330	
Thr Phe Ser Pro	Pro Leu Pro Arg His	Met Gln Glu Ala Leu	Arg
335	340	345	
Arg Leu His Tyr	Val Pro Ala Thr Lys	Val Phe Leu Ser Phe	Arg
350	355	360	
Arg Pro Phe Trp	Arg Glu Glu His Ile	Glu Gly Gly His Ser	Asn
365	370	375	
Thr Asp Arg Pro	Ser Arg Met Ile Phe	Tyr Pro Pro Pro Arg	Glu
380	385	390	
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr	Trp Ser Asp Ala Ala	Ala
395	400	405	
Ala Phe Ala Gly	Leu Ser Arg Glu Glu	Ala Leu Arg Leu Ala	Leu
410	415	420	
Asp Asp Val Ala	Ala Leu His Gly Pro	Val Val Arg Gln Leu	Trp
425	430	435	
Asp Gly Thr Gly	Val Val Lys Arg Trp	Ala Glu Asp Gln His	Ser
440	445	450	
Gln Gly Gly Phe	Val Val Gln Pro Pro	Ala Leu Trp Gln Thr	Glu

	455	460	465
Lys Asp Asp Trp	Thr Val Pro Tyr Gly	Arg Ile Tyr Phe Ala	Gly
	470	475	480
Glu His Thr Ala	Tyr Pro His Gly Trp	Val Glu Thr Ala Val	Lys
	485	490	495
Ser Ala Leu Arg	Ala Ala Ile Lys Ile	Asn Ser Arg Lys Gly	Pro
	500	505	510
Ala Ser Asp Thr	Ala Ser Pro Glu Gly	His Ala Ser Asp Met	Glu
	515	520	525
Gly Gln Gly His	Val His Gly Val Ala	Ser Ser Pro Ser His	Asp
	530	535	540
Leu Ala Lys Glu	Glu Gly Ser His Pro	Pro Val Gln Gly Gln	Leu
	545	550	555
Ser Leu Gln Asn	Thr Thr His Thr Arg	Thr Ser His	
	560	565	

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
 ctgacatggc ctgactcggg acagctcaga gcagggcaga actggggaca 50
 ctctgggccg gccttctgcc tgcattggacg ctctgaagcc accctgtctc 100
 tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcaggaa 150
 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200
 cccctcgcga gggctctgaat ttctctgtgc tgttcacaaa gatgcttttt 250
 atctttaact ttttgttttc ccacttccg accccggcgt tgatctgcat 300
 cctgacattt ggagctgcc tcttcttgtg gctgatcacc agacctcaac 350
 ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggga 400
 ggagcacgga aggggggttc ccagaagaac aatgacctaa caagttgctg 450
 cttctcagat gccaaagacta tgtatgaggt tttccaaaga ggactcgctg 500
 tgtctgacaa tgggccctgc ttgggatata gaaaaccaa ccagccctac 550
 agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600
 ctgtctcttg cataaagggt ataatcatc accagaccag tttgtcggca 650
 tctttgctca gaataggcca gagtggatca tctccgaatt ggcttggtac 700
 acgtactcta tggtagctgt acctctgtat gacaccttgg gaccagaagc 750

catcgtacat attgtcaaca aggctgatat cgccatggtg atctgtgaca 800
caccceaaaa ggcattggtg ctgataggga atgtagagaa aggcttcacc 850
ccgagcctga aggtgatcat ccttatggac ccctttgatg atgacctgaa 900
gcaaagaggg gagaagagtg gaattgagat cttatcccta tatgatgctg 950
agaacctagg caaagagcac ttcagaaaac ctgtgcctcc tagcccagaa 1000
gacctgagcg tcatctgctt caccagtggg accacaggtg accccaaagg 1050
agccatgata acccatcaaa atattgtttc aaatgctgct gcctttctca 1100
aatgtgtgga gcatgcttat gagcccactc ctgatgatgt ggccatatcc 1150
tacctccctc tggctcatat gtttgagagg attgtacagg ctggtgtgta 1200
cagctgtgga gccagagttg gattcttcca aggggatatt cggttgctgg 1250
ctgacgacat gaagactttg aagcccacat tgtttccgc ggtgcctcga 1300
ctccttaaca ggatctacga taaggtaaa aatgaggcca agacaccctt 1350
gaagaagttc ttgttgaagc tggctgtttc cagtaaattc aaagagcttc 1400
aaaaggggat catcaggcat gatagtttct gggacaagct catctttgca 1450
aagatccagg acagcctggg cggaagggtt cgtgtaattg tcaactggagc 1500
tgcccccattg tccacttcag tcatgacatt cttccgggca gcaatgggat 1550
gtcagggtgta tgaagcttat ggtcaaacag aatgcacagg tggctgtaca 1600
tttacattac ctggggactg gacatcaggt cacgttgggg tgcccctggc 1650
ttgcaattac gtgaagctgg aagatgtggc tgacatgaac tactttacag 1700
tgaataatga aggagaggtc tgcacaaagg gtacaaacgt gttcaaagga 1750
tacctgaagg accctgagaa gacacaggaa gccctggaga gtgatggctg 1800
gcttcacaca ggagacattg gtcgctggct cccgaatgga actctgaaga 1850
tcatcgaccg taaaaagaac attttcaagc tggcccaagg agaatacatt 1900
gcaccagaga agatagaaaa tatctacaac aggagtcaac cagtgttaca 1950
aatTTTTgta cacggggaga gcttacggtc atccttagta ggagtgggtg 2000
ttcctgacac agatgtactt ccctcatttg cagccaagct tgggggtgaag 2050
ggctcctttg aggaactgtg ccaaaaccaa gttgtaaggg aagccatttt 2100
agaagacttg cagaaaattg ggaaagaaag tggccttaaa acttttgaac 2150
agggtcaaagc catttttctt catccagagc cattttccat tgaaaatggg 2200

ctcttgacac caacattgaa agcaaagcga ggagagcttt ccaaatactt 2250
 tcggacccaa attgacagcc tgtatgagca catccaggat taggataagg 2300
 tacttaagta cctgccggcc cactgtgcac tgcttgtgag aaaatggatt 2350
 aaaaactatt cttacatttg ttttgccctt cctcctatct tttttaacc 2400
 tgttaaactc taaagccata gcttttgctt tatattgaga catataatgt 2450
 gttaaacttag ttcccaaata aatcaatcct gtctttccca tcttcgatgt 2500
 tgctaataatt aaggcttcag ggctactttt atcaacatgc ctgtcttcaa 2550
 gatcccagtt tatgttctgt gtccttcctc atgatttcca accttaatac 2600
 tattagtaac cacaagttca aggggtcaaag ggaccctctg tgccttcttc 2650
 tttgttttgt gataaacata acttgccaac agtctctatg cttatttaca 2700
 tcttctactg ttcaaactaa gagattttta aattctgaaa aactgcttac 2750
 aattcatggt ttctagccac tccacaaacc actaaaattt tagtttttagc 2800
 ctatcactca tgtcaatcat atctatgaga caaatgtctc cgatgctctt 2850
 ctgcgtaaatt taaattgtgt actgaaggga aaagtttgat cataccaaac 2900
 atttcctaaa ctctctagtt agatatctga cttgggagta ttaaaaattg 2950
 ggtctatgac atactgtcca aaaggaatgc tgttcttaaa gcattattta 3000
 cagtaggaac tggggagtaa atctgttccc tacagtttgc tgctgagctg 3050
 gaagctgtgg gggaaggagt tgacaggtgg gccagtgaa cttttccagt 3100
 aatgaagca agcactgaat aaaaacctcc tgaactggga acaaagatct 3150
 acaggcaagc aagatgccca cacaacaggc ttattttctg tgaaggaacc 3200
 aactgatctc cccaccctt ggattagagt tctgctcta ccttaccac 3250
 agataacaca tgttgcttct acttgtaaat gtaaagtctt taaaataaac 3300
 tattacagat aaaaaa 3316

<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

Met	Asp	Ala	Leu	Lys	Pro	Pro	Cys	Leu	Trp	Arg	Asn	His	Glu	Arg
1				5					10					15

Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
				20					25					30

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser		35	40	45
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile		50	55	60
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys		65	70	75
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg		80	85	90
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val		95	100	105
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn		110	115	120
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu		125	130	135
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu		140	145	150
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys		155	160	165
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His		170	175	180
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala		185	190	195
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr		200	205	210
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu		215	220	225
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile		230	235	240
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu		245	250	255
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro		260	265	270
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu		275	280	285
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe		290	295	300
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys		305	310	315
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr				

320					325					330				
His	Gln	Asn	Ile	Val	Ser	Asn	Ala	Ala	Ala	Phe	Leu	Lys	Cys	Val
				335					340					345
Glu	His	Ala	Tyr	Glu	Pro	Thr	Pro	Asp	Asp	Val	Ala	Ile	Ser	Tyr
				350					355					360
Leu	Pro	Leu	Ala	His	Met	Phe	Glu	Arg	Ile	Val	Gln	Ala	Val	Val
				365					370					375
Tyr	Ser	Cys	Gly	Ala	Arg	Val	Gly	Phe	Phe	Gln	Gly	Asp	Ile	Arg
				380					385					390
Leu	Leu	Ala	Asp	Asp	Met	Lys	Thr	Leu	Lys	Pro	Thr	Leu	Phe	Pro
				395					400					405
Ala	Val	Pro	Arg	Leu	Leu	Asn	Arg	Ile	Tyr	Asp	Lys	Val	Gln	Asn
				410					415					420
Glu	Ala	Lys	Thr	Pro	Leu	Lys	Lys	Phe	Leu	Leu	Lys	Leu	Ala	Val
				425					430					435
Ser	Ser	Lys	Phe	Lys	Glu	Leu	Gln	Lys	Gly	Ile	Ile	Arg	His	Asp
				440					445					450
Ser	Phe	Trp	Asp	Lys	Leu	Ile	Phe	Ala	Lys	Ile	Gln	Asp	Ser	Leu
				455					460					465
Gly	Gly	Arg	Val	Arg	Val	Ile	Val	Thr	Gly	Ala	Ala	Pro	Met	Ser
				470					475					480
Thr	Ser	Val	Met	Thr	Phe	Phe	Arg	Ala	Ala	Met	Gly	Cys	Gln	Val
				485					490					495
Tyr	Glu	Ala	Tyr	Gly	Gln	Thr	Glu	Cys	Thr	Gly	Gly	Cys	Thr	Phe
				500					505					510
Thr	Leu	Pro	Gly	Asp	Trp	Thr	Ser	Gly	His	Val	Gly	Val	Pro	Leu
				515					520					525
Ala	Cys	Asn	Tyr	Val	Lys	Leu	Glu	Asp	Val	Ala	Asp	Met	Asn	Tyr
				530					535					540
Phe	Thr	Val	Asn	Asn	Glu	Gly	Glu	Val	Cys	Ile	Lys	Gly	Thr	Asn
				545					550					555
Val	Phe	Lys	Gly	Tyr	Leu	Lys	Asp	Pro	Glu	Lys	Thr	Gln	Glu	Ala
				560					565					570
Leu	Asp	Ser	Asp	Gly	Trp	Leu	His	Thr	Gly	Asp	Ile	Gly	Arg	Trp
				575					580					585
Leu	Pro	Asn	Gly	Thr	Leu	Lys	Ile	Ile	Asp	Arg	Lys	Lys	Asn	Ile
				590					595					600
Phe	Lys	Leu	Ala	Gln	Gly	Glu	Tyr	Ile	Ala	Pro	Glu	Lys	Ile	Glu
				605					610					615

Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
				620					625					630
Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
				635					640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650					655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
				665					670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680					685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695					700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
				710					715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
				725					730					735

His Ile Gln Asp

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
 ggaggcggag gccgcggcga gccgggccga gcagtgaggg ccctagcggg 50
 gcccagcggg ggcccggggc ccctaagcca ttcctgaagt catgggctgg 100
 ccaggacatt ggtgaccgc caatccggta tggacgactg gaagcccagc 150
 cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200
 ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250
 cagggggcgt gcttttctg ctggtgactg tcattgtcaa tatcaagttg 300
 atcctggaca ctgcggcagc catcagtga gccaatgaag acccagagcc 350
 agagcaagac tatgatgagg ccctaggccg cctggagccc ccacggcgca 400
 gaggcagtgg tccccggcgg gtcctggacg tagaggtgta ttcaagtcgc 450
 agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggatgaggg 500
 ccgggagcag ggccggggca tccatgtcat tgtcctcaac caggccacgg 550
 gccacgtgat ggcaaaacgt gtgtttgaca cgtactcacc tcatgaggat 600
 gaggccatgg tgctattcct caacatggta gcgcccggcc gagtgctcat 650

ctgcactgtc aaggatgagg gtccttcca cctcaaggac acagccaagg 700
 ctctgctgag gagcctgggc agccaggctg gccctgccct gggctggagg 750
 gacacatggg ccttcgtggg acgaaaagga ggtcctgtct tcggggagaa 800
 acattctaag tcacctgccc tctcttctg gggggaccca gtcctgctga 850
 agacagatgt gccattgagc tcagcagaag aggcagagtg ccaactgggca 900
 gacacagagc tgaaccgtcg ccgccggcgc ttctgcagca aagttgaggg 950
 ctatggaagt gtatgcagct gcaaggaccc cacacccatc gagttcagcc 1000
 ctgacccact ccagacaac aaggctctca atgtgcctgt ggctgtcatt 1050
 gcagggaacc gaccaatta cctgtacagg atgctgcgct ctctgctttc 1100
 agcccagggg gtgtctctc agatgataac agttttcatt gacggctact 1150
 atgaggaacc catggatgtg gtggcactgt ttggtctgag gggcatccag 1200
 catactocca tcagcatcaa gaatgccgc gtgtctcagc actacaaggc 1250
 cagcctcact gccactttca acctgtttcc ggaggccaag tttgctgtgg 1300
 ttctggaaga ggacctggac attgctgtgg attttttcag tttcctgagc 1350
 caatccatcc acctactgga ggaggatgac agcctgtact gcactctctgc 1400
 ctggaatgac caggggtatg aacacacggc tgaggacca gcactactgt 1450
 accgtgtgga gaccatgcct gggctgggct gggtgctcag gaggtccttg 1500
 tacaaggagg agcttgagcc caagtggcct acaccgaaa agctctggga 1550
 ttgggacatg tggatgcgga tgcctgaaca acgccggggc cgagagtgca 1600
 tcatccctga cgtttccga tctaccact ttggcatcgt cggcctcaac 1650
 atgaatggct actttcacga ggcctacttc aagaagcaca agttcaacac 1700
 ggttccaggt gtccagctca ggaatgtgga cagtctgaag aaagaagctt 1750
 atgaagtgga agttcacagg ctgctcagt aggctgaggt tctggaccac 1800
 agcaagaacc cttgtgaaga ctcttctctg ccagacacag agggccacac 1850
 ctacgtggcc tttattcgaa tggagaaaga tgatgacttc accacctgga 1900
 ccagcttgc caagtgcctc catatctggg acctggatgt gcgtggcaac 1950
 catcggggcc tgtggagatt gtttcggaag aagaaccact tcctggtggt 2000
 gggggctccg gcttccccct actcagtga gaagccaccc tcagtcaccc 2050
 caattttcct ggagccaccc ccaaggagg agggagcccc aggagcccca 2100

gaacagacat gagacctcct ccaggaccct gcggggctgg gtactgtgta 2150
 cccccaggct ggctagccct tccctccatc ctgtaggatt ttgtagatgc 2200
 tggtaggggc tggggctacc ttgtttttaa catgagactt aattactaac 2250
 tccaagggga gggttcccct gctccaacac cccgttcctg agttaaagt 2300
 ctattttattt acttccttgt tggagaaggg caggagagta cctgggaatc 2350
 attacgatcc ctagcagctc atcctgccct ttgaataccc tcactttcca 2400
 ggcctggctc agaatctaac ctattttattg actgtcctga gggccttgaa 2450
 aacaggccga acctggaggg cctggatttc tttttgggct ggaatgctgc 2500
 cctgaggggtg gggctggctc ttactcagga aactgctgtg cccaacccat 2550
 ggacaggccc agctggggcc cacatgctga cacagactca ctcagagacc 2600
 cttagacact ggaccaggcc tcctctcagc cttctctttg tccagatttc 2650
 caaagctgga taagtgggtc attgattaaa aaaggagaag ccctctggga 2700
 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 88
 Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala
 1 5 10 15
 Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr
 20 25 30
 Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu
 35 40 45
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
 110 115 120
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
 125 130 135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val	380	385	390
Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe	395	400	405
Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr	410	415	420
Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu			

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly 440 445 450		
Trp Val Leu Arg Arg Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys 455 460 465		
Trp Pro Thr Pro Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg 470 475 480		
Met Pro Glu Gln Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val 485 490 495		
Ser Arg Ser Tyr His Phe Gly Ile Val Gly Leu Asn Met Asn Gly 500 505 510		
Tyr Phe His Glu Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val 515 520 525		
Pro Gly Val Gln Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala 530 535 540		
Tyr Glu Val Glu Val His Arg Leu Leu Ser Glu Ala Glu Val Leu 545 550 555		
Asp His Ser Lys Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr 560 565 570		
Glu Gly His Thr Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp 575 580 585		
Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp 590 595 600		
Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe 605 610 615		
Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro 620 625 630		
Tyr Ser Val Lys Lys Pro Pro Ser Val Thr Pro Ile Phe Leu Glu 635 640 645		
Pro Pro Pro Lys Glu Glu Gly Ala Pro Gly Ala Pro Glu Gln Thr 650 655 660		

<210> 89

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

gatggcaaaa cgtgtgtttg acacg 25

<210> 90
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 90
cctcaaccag gccacgggcc ac 22

<210> 91
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 91
cccaggcaga gatgcagtac aggc 24

<210> 92
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 92
cctccagtag gtggatggat tggctc 26

<210> 93
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 93
ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens

<400> 94

cggacgcgtg ggctgctggt gggaaggcct aaagaactgg aaagcccact 50
ctcttggaaac caccacacct gtttaaagaa cctaagcacc atttaaagcc 100
actggaaatt tgttgtctag tggttgtggg tgaataaagg agggcagaat 150
ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 200
gttacgtggc cggaatcatt cccttggctg ttaatttctc agaggaacga 250
ctgaagctgg tgactgtttt ggggtgctggc cttctctgtg gaactgctct 300
ggcagtcatc gtgcctgaag gagtacatgc cttttatgaa gatattcttg 350
agggaaaaca ccaccaagca agtgaaacac ataatgtgat tgcacagac 400
aaagcagcag aaaaatcagt tgtccatgaa catgagcaca gccacgacca 450
cacacagctg catgcctata ttggtgtttc cctcgttctg ggcttcgttt 500
tcatgttgct ggtggaccag attggtaact cccatgtgca ttctactgac 550
gatccagaag cagcaaggtc tagcaattcc aaaatcacca ccacgctggg 600
tctggttgtc catgctgcag ctgatggtgt tgctttggga gcagcagcat 650
ctacttcaca gaccagtgtc cagttaattg tgtttgtggc aatcatgcta 700
cataaggcac cagctgcttt tggactgggt tccttcttga tgcagctgg 750
cttagagcgg aatcgaatca gaaagcactt gctggctctt gcattggcag 800
caccagttat gtccatggtg acatacttag gactgagtaa gagcagtaaa 850
gaagcccttt cagaggtgaa cgccacggga gtggccatgc ttttctctgc 900
cgggacattt ctttatgttg ccacagtaca tgtcctccct gaggtgggag 950
gaatagggca cagccacaag cccgatgcca cgggaggag aggcctcagc 1000
cgctggaag tggcagccct ggttctgggt tgcctcatcc ctctcatcct 1050
gtcagtagga caccagcatt aaatgttcaa ggtccagcct tggccaggg 1100
ccgtttgcc aacagtgaga acagccggca cgtgacagct actcacttcc 1150
tcagtctctt gtctcacctt gcgcatctct acatgtattc ctagagtcca 1200
gaggggaggt gaggttaaaa cctgagtaat ggaaaagctt ttagagtaga 1250
aacacattta cgttgagtt agctatagac atcccattgt gttatctttt 1300
aaaaggccct tgacattttg cgttttaata tttctcttaa ccctattctc 1350
agggaaagatg gaatttagtt ttaaggaaaa gaggagaact tcatactcac 1400
aatgaaatag tgattatgaa aatacagtgt tctgtaatta agctatgtct 1450

ctttcttctt agtttagagg ctctgctact ttatccattg atttttaaca 1500
tggttccac catgtaagac tgggtgcttta gcatctatgc cacatgcgtt 1550
gatggaaggt catagcacc actcacttag atgctaaagg tgattctagt 1600
taatctggga ttagggtcag gaaaatgata gcaagacaca ttgaaagctc 1650
tctttatact caaaagagat atccattgaa aagggatgtc tagagggatt 1700
taaacagctc ctttggcacg tgcctctctg aatccagcct gccattccat 1750
caaatggagc aggagaggtg ggaggagctt ctaaagaggt gactggtatt 1800
ttgtagcatt ccttgtcaag ttctcctttg cagaatacct gtctccacat 1850
tcctagagag gagccaagtt ctagtagttt cagttctagg ctttccttca 1900
agaacagtca gatcaciaag tgtctttgga aattaaggga tattaattt 1950
taagtgattt ttgatgggt attgatattt ttgtagtagc tttttttaa 2000
agactaccaa aatgtatggt tgtccttttt tttgttttt tttttttta 2050
attatttctc ttagcagatc agcaatccct ctagggacct aaatactagg 2100
tcagctttgg cgacactgtg tcttctcaca taaccacctg tagcaagatg 2150
gatcataaat gagaagtgtt tgcctattga tttaaagctt attggaatca 2200
tgtctcttgt ctcttcgtct tttctttgct tttcttctaa cttttccctc 2250
tagcctctcc tcgccacaat ttgctgctta ctgctgggtg taatatttgt 2300
gtgggatgaa ttcttatcag gacaaccact tctcgaactg taataatgaa 2350
gataataata tctttattct ttatccccct caaagaaatt acctttgtgt 2400
caaatgccgc tttgttgagc ccttaaaata ccacctcctc atgtgtaaat 2450
tgacacaatc actaatctgg taatttaaac aattgagaça gcaaaagtgt 2500
ttaacagact aggataattt ttttttcata tttgccaaaa tttttgtaaa 2550
ccctgtcttg tcaaataagt gtataatatt gtattattaa tttattttta 2600
ctttctatac catttcaaaa cacattacac taagggggaa ccaagactag 2650
tttcttcagg gcagtggacg tagtagtttg taaaaacgtt ttctatgacg 2700
cataagctag catgcctatg atttatttcc ttcatgaatt tgtcactgga 2750
tcagcagctg tggaaataaa gcttgtagc cctctgctgg ccacagttag 2800
gaaagtagca caaataggat acagttgtat gtagtcattg gcaacaattg 2850
catacaattt tactaccaag agaaggtata gtatggaaag tccaaatgac 2900

ttccttgatt ggatgttaac agctgactgg tgtgagactt gaggtttcat 2950
 ctagtccttc aaaactatat gggtgcctag attctctctg gaaactgact 3000
 ttgtcaaata aatagcagat tgtagtgtca aaaaaaa 3037

<210> 95
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 95
 Met Asp Asp Phe Ile Ser Ile Ser Leu Leu Ser Leu Ala Met Leu
 1 5 10 15
 Val Gly Cys Tyr Val Ala Gly Ile Ile Pro Leu Ala Val Asn Phe
 20 25 30
 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu
 35 40 45
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
 50 55 60
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
 65 70 75
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
 95 100 105
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
 110 115 120
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
 125 130 135
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
 140 145 150
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
 155 160 165
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
 170 175 180
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
 185 190 195
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
 200 205 210
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
 215 220 225
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

	230	235	240
Asn Ala Thr Gly	Val Ala Met Leu Phe	Ser Ala Gly Thr Phe	Leu
	245	250	255
Tyr Val Ala Thr	Val His Val Leu Pro	Glu Val Gly Gly Ile	Gly
	260	265	270
His Ser His Lys	Pro Asp Ala Thr Gly	Gly Arg Gly Leu Ser	Arg
	275	280	285
Leu Glu Val Ala	Ala Leu Val Leu Gly	Cys Leu Ile Pro Leu	Ile
	290	295	300
Leu Ser Val Gly	His Gln His		
	305		

<210> 96
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 96
 gttgtgggtg aataaaggag ggcag 25

<210> 97
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 97
 ctgtgctcat gttcatggac aactg 25

<210> 98
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 98
 ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 50

<210> 99
 <211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

gctcgaggcc ggcggcggcg ggagagcgac ccgggcggcc tcgtagcggg 50
gccccggatc cccgagtggc ggccggagcc tcgaaaagag attctcagcg 100
ctgatTTtga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150
ccgccccctcg tgctggccgc cctggtggcc tgcattcatcg tcttgggctt 200
caactactgg attgcgagct cccggagcgt ggacctccag acacggatca 250
tgagactgga aggcagggtc cgcagggcgg ctgcagagag aggcgccgtg 300
gagctgaaga agaacgagtt ccagggagag ctggagaagc agcgggagca 350
gcttgacaaa atccagtcca gccacaactt ccagctggag agcgtcaaca 400
agctgtacca ggacgaaaag gcggttttgg tgaataacat caccacaggt 450
gagaggctca tccgagtgtt gcaagaccag ttaaagaccc tgcagaggaa 500
ttacggcagg ctgcagcagg atgtcctcca gtttcagaag aaccagacca 550
acctggagag gaagttctcc tacgacctga gccagtgcatt caatcagatg 600
aaggaggtga aggaacagtg tgaggagcga atagaagagg tcaccaaaaa 650
ggggaatgaa gctgtagctt ccagagacct gactgaaaac aacgaccaga 700
gacagcagct ccaagccctc agtgagcctc agcccaggct gcaggcagca 750
ggcctgccac acacagaggt gccacaaggg aagggaacg tgcttggtaa 800
cagcaagtcc cagacaccag cccccagttc cgaagtgggt ttggattcaa 850
agagacaagt tgagaaagag gaaaccaatg agatccaggt ggtgaatgag 900
gagcctcaga gggacaggct gccgcaggag ccaggccggg agcaggtggt 950
ggaagacaga cctgtaggtg gaagaggctt cgggggagcc ggagaactgg 1000
gccagacccc acaggtgcag gctgccctgt cagtgcagca ggaaaatcca 1050
gagatggagg gccctgagcg agaccagctt gtcattcccc acggacagga 1100
ggaggagcag gaagctgccg gggaaggag aaaccagcag aaactgagag 1150
gagaagatga ctacaacatg gatgaaaatg aagcagaatc tgagacagac 1200
aagcaagcag ccctggcagg gaatgacaga aacatagatg tttttaatgt 1250
tgaagatcag aaaagagaca ccataaattt acttgatcag cgtgaaaagc 1300
ggaatcatac actctgaatt gaactggaat cacatatattt acaacagggc 1350

cgaagagatg actataaaat gttcatgagg gactgaatac tgaaaactgt 1400

gaaatgtact aaataaaatg tacatctga 1429

<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

Met	Met	Gly	Leu	Gly	Asn	Gly	Arg	Arg	Ser	Met	Lys	Ser	Pro	Pro
1				5					10					15

Leu	Val	Leu	Ala	Ala	Leu	Val	Ala	Cys	Ile	Ile	Val	Leu	Gly	Phe
			20						25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
			35						40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
			50						55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
			65						70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
			80						85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
			95						100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
			110						115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
			125						130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
			140						145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
			155						160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
			170						175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
			185						190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
			200						205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
			215						220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
			230						235					240

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr	245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu	260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val	275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro	290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met	305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu	335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	380	385	390
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu	395	400	

<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

<400> 101
 ggatgcagaa agcctcagtg ttgctcttcc tggcctgggt ctgcttcctc 50
 ttctacgctg gcattgccct cttcaccagt ggcttcctgc tcacccgttt 100
 ggagctcacc aaccatagca gctgccaaga gccccaggc cctgggtccc 150
 tgccatgggg gagccaaggg aaacctgggg cctgctggat ggcttcccga 200
 ttttcgcggg ttgtgttggg gctgatagat gctctgcgat ttgacttcgc 250
 ccagccccag cattcacacg tgcctagaga gcctcctgtc tccctaccct 300
 tcctgggcaa actaagctcc ttgcagagga tcctggagat tcagccccac 350
 catgcccggc tctaccgatc tcaggttgac cctcctacca ccaccatgca 400
 gcgcctcaag gccctcacca ctggctcact gcctaccttt attgatgctg 450
 gtagtaactt cgccagccac gccatagtgg aagacaatct cattaagcag 500

ctcaccagtg caggaaggcg tgtagtcttc atgggagatg atacctggaa 550
 agaccttttc cctggtgctt tctccaaagc tttcttcttc ccattccttca 600
 atgtcagaga cctagacaca gtggacaatg gcattcctgga acacctctac 650
 cccaccatgg acagtgggta atgggacgtg ctgattgctc acttcctggg 700
 tgtggaccac tgtggccaca agcatggccc tcaccaccct gaaatggcca 750
 agaaacttag ccagatggac caggtgatcc agggacttgt ggagcgtctg 800
 gagaatgaca cactgctggt agtggctggg gaccatggga tgaccacaaa 850
 tggagaccat ggaggggaca gtgagctgga ggtctcagct gctctctttc 900
 tgtatagccc cacagcagtc ttccccagca cccaccaga ggagccagag 950
 gtgattcctc aagttagcct tgtgccacg ctggccctgc tgetgggcct 1000
 gcccatccca tttgggaata tcggggaagt gatggctgag ctattctcag 1050
 ggggtgagga ctcccagccc cactcctctg ctttagccca agcctcagct 1100
 ctccatctca atgtcagca ggtgtccga tttcttcata cctactcagc 1150
 tgctactcag gacctcaag ctaaggagct tcattcagct cagaacctct 1200
 tctccaaggc ctctgctgac taccagtggc ttctccagag cccaagggg 1250
 gctgaggcga cactgccgac tgtgattgct gagctgcagc agttcctgcg 1300
 gggagctcgg gccatgtgca tcgagtcttg ggctcgtttc tctctggctc 1350
 gcatggcggg gggactgct ctcttggtg cttcctgctt tatctgcctg 1400
 ctggcatctc agtgggcaat atccccaggc tttccattct gccctctact 1450
 cctgacacct gtggcctggg gcctgggttg ggccatagcg tatgctggac 1500
 tcctgggaac tattgagctg aagctagatc tagtgcttct aggggctgtg 1550
 gctgcagtga gctattcct ccttttctg tggaaagcct gggctggctg 1600
 ggggtccaag agggccctgg caaccctgtt tccatccct gggcccgctc 1650
 tgttactcct gctgtttcgc ttggctgtgt tcttctctga tagttttgtt 1700
 gtagctgagg ccagggccac ccccttcctt ttgggctcat tcattcctgct 1750
 cctggttgct cagcttcact gggagggcca gctgcttcca cctaagctac 1800
 tcacaatgcc ccgccttggc acttcagcca caacaaaccc cccacggcac 1850
 aatggtgcat atgcctgag gcttggaatt ggggtgcttt tatgtacaag 1900
 gctagctggg ctttttcatt gttgccctga agagacacct gtttgccact 1950

cctctccctg gctgagtcct ctggcatcca tgggtgggtgg tcgagccaag 2000
aatttatggg atggagcttg tgtggcggcg ctgggtggccc tgtagctgc 2050
cgtgcgcttg tggttcgcc gctatggtaa tctcaagagc cccgagccac 2100
ccatgctctt tgtgcgctgg ggactgcccc taatggcatt gggtagctgt 2150
gcctactggg cattggcgtc gggggcagat gaggtcctccc cccgtctccg 2200
ggtcctgggtc tctggggcat ccatgggtgt gcctcgggct gtagcagggc 2250
tggtgtcttc agggctcgcg ctgctgtctt ggaagcctgt gacagtgtgt 2300
gtgaaggctg gggcaggcgc tccaaggacc aggactgtcc tcaactccctt 2350
ctcaggcccc cccacttctc aagctgactt ggattatgtg gtccctcaaa 2400
tctaccgaca catgcaggag gaggttccgg gccgggttaga gaggaccaa 2450
tctcagggtc cctgactgt ggctgttat cagttgggga gtgtctactc 2500
agctgtatg gtcacagccc tcacctgtt ggcttccca cttctgtgt 2550
tgcatgcga gcgcacagc cttgtgttcc tgcttctgtt tctgcagagc 2600
ttccttctcc tacatctgt tgctgtggg ataccgtca ccacctctg 2650
tccttttact gtgccatggc aggcagtctc ggcttgggcc ctcattggcca 2700
cacagacctt ctactccaca ggccaccagc ctgtcttcc agccatccat 2750
tggcatgcag ccttcgtggg attcccagag ggtcatggct cctgtacttg 2800
gctgcctgt ttgctagtgg gagccaacac ctttgctcc cacctcctct 2850
ttgcagtagg ttgccactg ctctgtctt ggcttttct gtgtgagagt 2900
caagggctgc ggaagagaca gcagccccc ggaatgaag ctgatgccag 2950
agtcagacc gaggaggaag aggagccact gatggagatg cggctccggg 3000
atgcgcctca gcacttctat gcagcactgc tgcagctggg cctcaagtac 3050
ctctttatcc ttggtattca gattctggc tgtgccttg cagcctccat 3100
ccttcgcagg catctcatgg tctggaaagt gtttgcccct aagttcatat 3150
ttgaggctgt gggcttcatt gtgagcagcg tgggacttct cctgggcata 3200
gcttttgtga tgagagtga tgggtgtgt agctcctgg tccaggcagct 3250
atctctggcc cagcagaggt agcctagtct gtgattactg gcacttggct 3300
acagagagt ctggagaaca gtgtagcctg gcctgtacag gtactggatg 3350
atctgcaaga caggctcagc catactctta ctatcatgca gccaggggcc 3400

gctgacatct aggacttcat tattctataa ttcaggacca cagtggagta 3450
 tgatccctaa ctctgatatt ggatgcatct gagggacaag gggggcggtc 3500
 tccgaagtgg aataaaatag gccgggcgtg gtgacttgca cctataatcc 3550
 cagcactttg ggaggcagag gtgggaggat tgcttgggtcc caggagtcca 3600
 agaccagcct gtggaacata acaagacccc gtctctacta tttaaaaaaa 3650
 agtgtaataa aatgataata t 3671

<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

Met	Gln	Lys	Ala	Ser	Val	Leu	Leu	Phe	Leu	Ala	Trp	Val	Cys	Phe	1	5	10	15
Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu	20	25	30	
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	35	40	45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	50	55	60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	65	70	75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	80	85	90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	95	100	105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	110	115	120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	125	130	135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	140	145	150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	155	160	165	
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	170	175	180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	185	190	195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly				

200										205					210				
Ile	Leu	Glu	His	Leu	Tyr	Pro	Thr	Met	Asp	Ser	Gly	Glu	Trp	Asp					
				215					220					225					
Val	Leu	Ile	Ala	His	Phe	Leu	Gly	Val	Asp	His	Cys	Gly	His	Lys					
				230					235					240					
His	Gly	Pro	His	His	Pro	Glu	Met	Ala	Lys	Lys	Leu	Ser	Gln	Met					
				245					250					255					
Asp	Gln	Val	Ile	Gln	Gly	Leu	Val	Glu	Arg	Leu	Glu	Asn	Asp	Thr					
				260					265					270					
Leu	Leu	Val	Val	Ala	Gly	Asp	His	Gly	Met	Thr	Thr	Asn	Gly	Asp					
				275					280					285					
His	Gly	Gly	Asp	Ser	Glu	Leu	Glu	Val	Ser	Ala	Ala	Leu	Phe	Leu					
				290					295					300					
Tyr	Ser	Pro	Thr	Ala	Val	Phe	Pro	Ser	Thr	Pro	Pro	Glu	Glu	Pro					
				305					310					315					
Glu	Val	Ile	Pro	Gln	Val	Ser	Leu	Val	Pro	Thr	Leu	Ala	Leu	Leu					
				320					325					330					
Leu	Gly	Leu	Pro	Ile	Pro	Phe	Gly	Asn	Ile	Gly	Glu	Val	Met	Ala					
				335					340					345					
Glu	Leu	Phe	Ser	Gly	Gly	Glu	Asp	Ser	Gln	Pro	His	Ser	Ser	Ala					
				350					355					360					
Leu	Ala	Gln	Ala	Ser	Ala	Leu	His	Leu	Asn	Ala	Gln	Gln	Val	Ser					
				365					370					375					
Arg	Phe	Leu	His	Thr	Tyr	Ser	Ala	Ala	Thr	Gln	Asp	Leu	Gln	Ala					
				380					385					390					
Lys	Glu	Leu	His	Gln	Leu	Gln	Asn	Leu	Phe	Ser	Lys	Ala	Ser	Ala					
				395					400					405					
Asp	Tyr	Gln	Trp	Leu	Leu	Gln	Ser	Pro	Lys	Gly	Ala	Glu	Ala	Thr					
				410					415					420					
Leu	Pro	Thr	Val	Ile	Ala	Glu	Leu	Gln	Gln	Phe	Leu	Arg	Gly	Ala					
				425					430					435					
Arg	Ala	Met	Cys	Ile	Glu	Ser	Trp	Ala	Arg	Phe	Ser	Leu	Val	Arg					
				440					445					450					
Met	Ala	Gly	Gly	Thr	Ala	Leu	Leu	Ala	Ala	Ser	Cys	Phe	Ile	Cys					
				455					460					465					
Leu	Leu	Ala	Ser	Gln	Trp	Ala	Ile	Ser	Pro	Gly	Phe	Pro	Phe	Cys					
				470					475					480					
Pro	Leu	Leu	Leu	Thr	Pro	Val	Ala	Trp	Gly	Leu	Val	Gly	Ala	Ile					
				485					490					495					

Ala Tyr Ala Gly	Leu Leu Gly Thr Ile	Glu Leu Lys Leu Asp	Leu
500	505	510	
Val Leu Leu Gly	Ala Val Ala Ala Val	Ser Ser Phe Leu Pro	Phe
515	520	525	
Leu Trp Lys Ala	Trp Ala Gly Trp Gly	Ser Lys Arg Pro Leu	Ala
530	535	540	
Thr Leu Phe Pro	Ile Pro Gly Pro Val	Leu Leu Leu Leu	Phe
545	550	555	
Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu	Ala
560	565	570	
Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu	Val
575	580	585	
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu	Leu
590	595	600	
Thr Met Pro Arg	Leu Gly Thr Ser Ala	Thr Thr Asn Pro Pro	Arg
605	610	615	
His Asn Gly Ala	Tyr Ala Leu Arg Leu	Gly Ile Gly Leu Leu	Leu
620	625	630	
Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu	Thr
635	640	645	
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser	Met
650	655	660	
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val	Ala
665	670	675	
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg	Arg
680	685	690	
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val	Arg
695	700	705	
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp	Ala
710	715	720	
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val	Leu
725	730	735	
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu
740	745	750	
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val
755	760	765	
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu
770	775	780	
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp	Tyr

785					790					795				
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met	Gln	Glu	Glu	Phe	Arg	Gly
				800										810
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly	Pro	Leu	Thr	Val	Ala	Ala
				815										825
Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala	Ala	Met	Val	Thr	Ala	Leu
				830										840
Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu	Leu	His	Ala	Glu	Arg	Ile
				845										855
Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu	Gln	Ser	Phe	Leu	Leu	Leu
				860										870
His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val	Thr	Thr	Pro	Gly	Pro	Phe
				875										885
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala	Trp	Ala	Leu	Met	Ala	Thr
				890										900
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln	Pro	Val	Phe	Pro	Ala	Ile
				905										915
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe	Pro	Glu	Gly	His	Gly	Ser
				920										930
Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val	Gly	Ala	Asn	Thr	Phe	Ala
				935										945
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys	Pro	Leu	Leu	Leu	Leu	Trp
				950										960
Pro	Phe	Leu	Cys	Glu	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Gln	Gln	Pro
				965										975
Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val	Arg	Pro	Glu	Glu	Glu	Glu
				980										990
Glu	Pro	Leu	Met	Glu	Met	Arg	Leu	Arg	Asp	Ala	Pro	Gln	His	Phe
				995										1005
Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu	Lys	Tyr	Leu	Phe	Ile	Leu
				1010										1020
Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg
				1025										1035
Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe
				1040										1050
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly
				1055										1065
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe
				1070										1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 103
tgccgctgcc gccgctgctg ctgttgetcc tggcggcgcc ttggggacgg 50
gcagttccct gtgtctctgg tggtttgcct aaacctgcaa acatcacctt 100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatcaaac agaacgtggc cccagtgtgt gaccaaccac acgctgggtc 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
aaaaaatcgt gattaacttt atcacctca atatctcgga tgattctaaa 750
atttctcatc aggatatgag ttactggga aaaagcagtg atgtatccag 800
ccttaatgat cctcagccca gcgggaacct gagggccct caggaggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtcctt 950
cagcagaaca atacccccg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcgtt 1100
ggcagtcttg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccc 1200
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300
 agccttctga gggggatggg ctcgagagag agggcttct atctagactc 1350
 tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct 1400
 catgcaattc atggaggaat ggggggttata tgtgcagatg gaaaactgat 1450
 gccaacactt ccttttgctt tttgtttcct gtgcaaaca gtgagtcacc 1500
 cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt 1550
 ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600
 cgtgtgtgat tggttcatgc atgtaggctt cttacaatg atgggtgggc 1650
 tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat 1700
 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104
 <211> 442
 <212> PRT
 <213> Homo sapiens

<400> 104
 Met Ser Tyr Asn Gly Leu His Gln Arg Val Phe Lys Glu Leu Lys
 1 5 10 15
 Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu
 20 25 30
 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
 35 40 45
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
 50 55 60
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
 65 70 75
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
 80 85 90
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
 95 100 105
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
 110 115 120
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
 125 130 135
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
 140 145 150
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
 155 160 165

Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile	170	175	180
Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys	185	190	195
Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys	200	205	210
Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val	215	220	225
Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro	230	235	240
Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu	245	250	255
Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser	260	265	270
Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys	275	280	285
Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys	290	295	300
Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser	305	310	315
Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu	320	325	330
Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp	335	340	345
Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro	350	355	360
Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr	365	370	375
Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser	380	385	390
Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly	395	400	405
Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro	410	415	420
Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly	425	430	435
Leu Tyr Val Gln Met Glu Asn	440		

<210> 105

<211> 21
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-21
 <223> Synthetic construct

 <400> 105
 cgctgctgct gttgctcctg g 21

 <210> 106
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 106
 cagtgtgcca ggactttg 18

 <210> 107
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 107
 agtcgcaggc agcgttgg 18

 <210> 108
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 108
 ctctccgag tctgtgtgct cctgc 25

 <210> 109
 <211> 51
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence

<222> 1-51
<223> Synthetic construct.

<400> 109
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacaat 50
c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
cggacgcgtg ggcggacgcg tgggcggacg cgtgggtctc tgcggggaga 50
cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100
tctgctgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150
gctcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250
cttctgctg cgagcccgt ggggtggtctc ggccgcccac tgcttcagcc 300
acagagacct ccgcactggc ctggtggtgc tgggcgcca cgtcctgagt 350
actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccagca 400
ccccgactac caccatga cccagccaa cgacatctgc ctgctgcggc 450
tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggtgcca 500
gggagaaggg ccaggcccc cacagcggg acacggtgcc ggggtggctgg 550
ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600
ccaaggtccg agtgcctggc ccggacgtct gcaacagctc ctggaagggc 650
cacctgacac ttacatgct ctgcaccgc agtggggaca gccacagacg 700
gggtttctgc tcggccgact ccggagggcc cctggtgtgc aggaaccggg 750
ctcacggcct cgtttccttc tcgggcctct ggtgcggcga cccaagacc 800
cccgacgtgt acacgcaggt gtccgccttt gtggcctgga tctgggacgt 850
ggttcggcgg agcagtcacc agcccgccc cctgcctggg accaccaggc 900
ccccaggaga agccgctga gccacaacct tgcggcatgc aaatgagatg 950
gccgctccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000
tgttcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050
tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111
<211> 283
<212> PRT
<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val	
1				5					10					15	
Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp	
				20					25					30	
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg	
			35						40					45	
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly	
				50					55					60	
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys	
				65					70					75	
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala	
				80					85					90	
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile	
				95					100					105	
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala	
				110					115					120	
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly	
				125					130					135	
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro	
				140					145					150	
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val	
				155					160					165	
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val	
				170					175					180	
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His	
				185					190					195	
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg	
				200					205					210	
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg	
				215					220					225	
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly	
				230					235					240	
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val	
				245					250					255	

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
 260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
 275 280

<210> 112
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 112
 gacgtctgca acagctcctg gaag 24

<210> 113
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 113
 cgagaaggaa acgaggccgt gag 23

<210> 114
 <211> 44
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-44
 <223> Synthetic construct.

<400> 114
 tgacacttac catgctctgc acccgagtg gggacagcca caga 44

<210> 115
 <211> 1808
 <212> DNA
 <213> Homo sapiens

<400> 115
 gagctacca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50
 cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100
 cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
 tatgtcaccg gtggggcttg ccccagcaag gccaccatcc ctgggaagac 200

ggtcatcgtg acgggcgcca acacaggcat cgggaagcag accgccttgg 250
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
 tgtcaacgcc cggcacctgg acttggcttc cctcaagtct atccgagagt 400
 ttgcagcaaa gatcattgaa gaggaggagc gaggggacat tctaataaac 450
 aacgcgggtg tgatgcgggtg cccccactgg accaccgagg acggcttcga 500
 gatgcagttt ggcgttaacc acctgggtca ctttctcttg aaaaacttgc 550
 tgctggacaa gctgaaagcc tcagcccctt cgcggatcat caacctctcg 600
 tccctggccc atgttgctgg gcacatagac ttgacgact tgaactggca 650
 gacgaggaag tataacacca aagccgccta ctgccagagc aagctcgcca 700
 tcgtcctctt caccaaggag ctgagccggc ggctgcaagg ctctggtgtg 750
 actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tgggcagaca 800
 cacgggcac ccatggctcca cttctccag caccacactc gggcccatct 850
 tctggctgct ggtaagagc cccgagctgg ccgcccagcc cagcacatac 900
 ctggccgtgg cggaggaact ggcggatgtt tccggaaagt acttcgatgg 950
 actcaaacag aaggccccgg cccccgaggc tgaggatgag gaggtggccc 1000
 ggaggctttg ggctgaaagt gccgcctgg tgggcttaga ggctccctct 1050
 gtgagggagc agccccctcc cagataacct ctggagcaga ttgaaagcc 1100
 aggatggcgc ctccagaccg aggacagctg tccgccatgc ccgagcttc 1150
 ctggcactac ctgagccggg agaccagga ctggcgggcc ccatgcccgc 1200
 agtaggttct agggggcggt gctggccgca gtggactggc ctgcaggtga 1250
 gcaactgccc gggctctggc tggttccgtc tgctctgctg ccagcagggg 1300
 agaggggcca tctgatgctt cccctgggaa tctaaactgg gaatggccga 1350
 ggaggaagg gctctgtgca cttgcaggcc acgtcaggag agccagcgg 1400
 gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450
 tctgacactt ggtggattct tgggtccctg tgggaccttg tgcatgcatg 1500
 gtctctctg agccttgggt tcttcagcag tgagatgctc agaataactg 1550
 ctgtctccca tgatgggtgt gtacagcgag ctgttgctg gctatggcat 1600
 ggctgtgccg ggggtgtttg ctgagggtt cctgtgccag agcccagcca 1650

gagagcaggt gcaggtgtca tcccgagttc aggctctgca cggcatggag 1700
 tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750
 caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800
 gctcattt 1808

<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116
 Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
 1 5 10 15
 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
 20 25 30
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230						235				240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

<400> 117
 gaagttcgcg agcgctggca tgtggtcctg gggcgcggtt ggcggcgctg 50
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100
 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150
 agcgccggtt gctggggctg ctgaggcggg acctgcgcgg ggaggaggcg 200
 cggctgcggg acctgactag attctacgac aaggtacttt ctttgcata 250
 ggattcaaca acccctgtgg ctaacctctt gcttgcattt acttcatca 300
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
 gagaacatcc gagctctgaa ggatggctat gagaagggtg agcaagacct 400
 tccagccttt gaggacctg agggagcagc aagggccctg atgcggctgc 450
 aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500
 agagtcaactg gctctgccat cactgacctg tacagcccca aacggctctt 550
 ttctctcaca ggggatgact gcttccaagt tggcaagggt gcctatgaca 600
 tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700

agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750
 cgtgtgccct cagcctctct cgggagtttc ttctctacag cccagataat 800
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850
 cccaaccac gtggtagctg aggtgtcat ccagaggccc aatatacccc 900
 acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950
 cagcccactc tctaccagat ccctagcctc tactgttctt atgagaccaa 1000
 ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcattccacc 1050
 tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100
 cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtggc 1150
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200
 ggctgaagga cactgttgac caaaactgg tgaccctcaa ccaccgcatt 1250
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350
 ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400
 gcaacattta tgatctatct gagctcgggt gaagctggag gagccacagc 1450
 ctteatctat gccaacctca gcgtgcctgt ggttaggaat gcagcactgt 1500
 tttggtggaa cctgcacagg agtgggtgaag gggacagtga cacacttcat 1550
 gctggctgtc ctgtcctggg gggagataag tgggtggcca acaagtggat 1600
 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650
 actgaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700
 aagccaggag caaaagctg gggtaggaga ggagaaagca gagcagcctc 1750
 ctggaagaag gccttgtcag ctttgtctgt gcctcgcaa tcagaggcaa 1800
 gggagagggt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850
 agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtggg 1900
 ggctgagag ggaagtttct ggagttcaga tactctctgt tggaacagg 1950
 acatctcaac agtctcaggt tcgatcagtg ggtcttttgg cactttgaac 2000
 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050
 tagcctgact ccagaactt taagactttc tccccactgc cttctgctgc 2100
 agcccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150

tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly	Asn	Val	Ser	Cys	Ala	Leu	Ser	Leu	Ser	Arg	Glu	Phe	Leu	Leu	
				245					250					255	
Tyr	Ser	Pro	Asp	Asn	Lys	Arg	Met	Ala	Arg	Asn	Val	Leu	Lys	Tyr	
				260					265					270	
Glu	Arg	Leu	Leu	Ala	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala	
				275					280					285	
Val	Ile	Gln	Arg	Pro	Asn	Ile	Pro	His	Leu	Gln	Thr	Arg	Asp	Thr	
				290					295					300	
Tyr	Glu	Gly	Leu	Cys	Gln	Thr	Leu	Gly	Ser	Gln	Pro	Thr	Leu	Tyr	
				305					310					315	
Gln	Ile	Pro	Ser	Leu	Tyr	Cys	Ser	Tyr	Glu	Thr	Asn	Ser	Asn	Ala	
				320					325					330	
Tyr	Leu	Leu	Leu	Gln	Pro	Ile	Arg	Lys	Glu	Val	Ile	His	Leu	Glu	
				335					340					345	
Pro	Tyr	Ile	Ala	Leu	Tyr	His	Asp	Phe	Val	Ser	Asp	Ser	Glu	Ala	
				350					355					360	
Gln	Lys	Ile	Arg	Glu	Leu	Ala	Glu	Pro	Trp	Leu	Gln	Arg	Ser	Val	
				365					370					375	
Val	Ala	Ser	Gly	Glu	Lys	Gln	Leu	Gln	Val	Glu	Tyr	Arg	Ile	Ser	
				380					385					390	
Lys	Ser	Ala	Trp	Leu	Lys	Asp	Thr	Val	Asp	Pro	Lys	Leu	Val	Thr	
				395					400					405	
Leu	Asn	His	Arg	Ile	Ala	Ala	Leu	Thr	Gly	Leu	Asp	Val	Arg	Pro	
				410					415					420	
Pro	Tyr	Ala	Glu	Tyr	Leu	Gln	Val	Val	Asn	Tyr	Gly	Ile	Gly	Gly	
				425					430					435	
His	Tyr	Glu	Pro	His	Phe	Asp	His	Ala	Thr	Ser	Pro	Ser	Ser	Pro	
				440					445					450	
Leu	Tyr	Arg	Met	Lys	Ser	Gly	Asn	Arg	Val	Ala	Thr	Phe	Met	Ile	
				455					460					465	
Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr	
				470					475					480	
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp	
				485					490					495	
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	
				500					505					510	
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys	
				515					520					525	
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser	

Ser Pro Glu Asp

<210> 119
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 119
cgggacagga gacccagaaa ggg 23

<210> 120
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 120
ggccaagtga tccaaggcat cttc 24

<210> 121
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-49
<223> Synthetic construct.

<400> 121
ctgcgggacc tgactagatt ctacgacaag gtactttcctt tgcattggg 49

<210> 122
<211> 1778
<212> DNA
<213> Homo sapiens

<400> 122
gagatagga gtctgggttt aagttcctgc tccatctcag gagccctgc 50
tcccaccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100
gaatcgggcc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150
ggagagcccc ggagccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250
 gctcaagttt tcacttatca tctattccac cgtgttcttg ctgattggg 300
 ccctggctct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
 aaaacccttg aaagtgcctt cctgggtcca gccatcatcc tcctcctct 400
 gggcgctcgt atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
 gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500
 ctcatcatgg agctcattgg tggcggtggg gccttgacct tccggaacca 550
 gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600
 atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650
 aagtgtgtgt gcggggagga ctaccgagat tggagcaaga atcagtacca 700
 cgactgcagt gccctggac ccctggcctg tggggtgccc tacacctgct 750
 gcatcaggaa cacgacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800
 atcgacaagg agcgtttcag tgtgcaggat gtcactctac tgcggggctg 850
 caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900
 gcatcctcct gggcatcctg ctccccagt tctgggggt gctgctgacg 950
 ctgctgtaca tcaccgggt ggaggacatc atcatggagc actctgtcac 1000
 tgatgggctc ctggggcccg gtgccaagcc cagcgtggag gcggcaggca 1050
 cgggatgctg cttgtgctac cccaattagg gccagcctg ccatggcagc 1100
 tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150
 ggacagggct gcggccctc tgcccacact cagtactgac caaagccagg 1200
 gctgtgtgtg cctgtgtgta ggtcccacgg cctctgctc cccagggagc 1250
 agagcctggg cctcccctaa gaggttttc ccgaggcagc tctggaatct 1300
 gtgcccacct ggggcctggg gaacaaggcc ctctttctc caggcctggg 1350
 ctacagggga gggagagcct gaggtctgc tcagggccca tttcatctct 1400
 ggcagtgcct tggcgggtgt attcaaggca gttttgtagc acctgtaatt 1450
 ggggagaggg agtgtgcccc tcggggcagg aggaagggc atctggggaa 1500
 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccaggttggc 1550
 ctcttctcag cctcccagg gccttgagcc ctcttgaag ggcggtgct 1600
 tcttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctgggtat ttccccgcat 1700
 gtcttattct tgcccttccc ccaaccagtt tgттаatcaa acaataaaaa 1750
 catgttttgt tttgttttta aaaaaaaa 1778

<210> 123
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 123
 Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe
 1 5 10 15
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
 20 25 30
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
 35 40 45
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
 50 55 60
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
 65 70 75
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
 80 85 90
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
 95 100 105
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
 110 115 120
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
 125 130 135
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
 140 145 150
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
 155 160 165
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
 170 175 180
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
 185 190 195
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
 200 205 210
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
 215 220 225
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

	230		235		240
Ile Leu Leu Pro	Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr			
	245	250			255
Ile Thr Arg Val	Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp			
	260	265			270
Gly Leu Leu Gly	Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly			
	275	280			285
Thr Gly Cys Cys	Leu Cys Tyr Pro Asn				
	290				

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
 cctgtctgtg ggcattctatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50
gctgccctct gacacctggg aagatggccg gcccgaggac cttcaccctt 100
ctctgtgggt tgctggcagc caccttgatc caagccaccc tcagtccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
ggtgaacacc gtctgaagc acatcatctg gctgaaggct atcacagcta 350
acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400
gtcaagatcc ccttgacat ggtggctgga ttcaacacgc ccttggtcaa 450
gaccatcgtg gagttccaca tgacgactga ggccaagcc accatccgca 500
tggacaccag tgcaagtggc cccaccgcc tggctctcag tgactgtgcc 550
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttcc 600
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagt ccatccctgc 650
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700
ggcatgtatg cagacctcct gcagctggtg aagggtgcca tttccctcag 750
cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca 800
ccattcagct ctacctgggg gccaaagttgt tggactcaca gggaaagggtg 850
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
caacatcccg ttcagcctca tcgtgagtca ggacgtggtg aaagctgcag 950
tggctgctgt gctctctcca gaagaattca tggctcctgtt ggactctgtg 1000
cttctgaga gtgccatcg gctgaagtca agcatcgggc tgatcaatga 1050
aaaggctgca gataagctgg gatctaccca gatcgtgaag atcctaactc 1100
aggacactcc cgagtttttt atagaccaag gccatgcca ggtggcccaa 1150
ctgatcgtgc tggaaagtgt tccctccagt gaagccctcc gccctttgtt 1200
caccctgggc atcgaagcca gctcggaagc tcagttttac accaaagggtg 1250
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
cactgagatc atccaactcca tctgctgcc gaaccagaat ggcaaattaa 1400
gatctggggt ccagtgatca ttggtgaagg ccttgggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttggtg cttactccag cctccttggtg 1500
 gaaacccagc tctcctgtct cccagtgaag acttggatgg cagccatcag 1550
 ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
 cctctctgca atcaataaac acttgcctgt gaaaaa 1636

<210> 128
 <211> 484
 <212> PRT
 <213> Homo sapiens

<400> 128
 Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala
 1 5 10 15
 Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile
 20 25 30
 Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
 35 40 45
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
 50 55 60
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
 65 70 75
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
 80 85 90
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
 95 100 105
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
 110 115 120
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
 125 130 135
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
 140 145 150
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
 155 160 165
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
 170 175 180
 Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
 185 190 195
 Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
 200 205 210
 Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
 215 220 225

Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys	
				230					235					240	
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser	
				245					250					255	
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu	
				260					265					270	
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser	
				275					280					285	
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu	
				290					295					300	
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His	
				305					310					315	
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp	
				320					325					330	
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr	
				335					340					345	
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu	
				350					355					360	
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu	
				365					370					375	
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr	
				380					385					390	
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp	
				395					400					405	
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp	
				410					415					420	
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu	
				425					430					435	
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu	
				440					445					450	
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys	
				455					460					465	
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser	
				470					475					480	

Pro Val Ser Gln

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129

gagcgaacat ggcagcgcggt tggcggtttt ggtgtgtctc tgtgaccatg 50
gtggtggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgccc aaag 100
aaagaaggag atggtgttat ctgaaaagggt tagtcagctg atggaatgga 150
ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200
gtgaaagccc caccgagaaa ttactccgtt atcgatcatgt tcaactgctct 250
ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300
agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350
ttttttgcca tgggtggattt tgatgaaggc tctgatgtat ttcagatgct 400
aaacatgaat tcagctccaa ctttcatcaa ctttctgca aaagggaaac 450
ccaaacgggg tgatacatat gagttacagg tgcgggggtt ttcagctgag 500
cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550
tagaccccca aattatgctg gtccccttat gttgggattg cttttggctg 600
ttattggtgg acttgtgtat cttcgaagaa gtaatatgga atttctcttt 650
aataaaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700
atctggtcaa atgtggaacc atataagagg accaccatat gcccataaga 750
atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800
ttttagctg aaacacacat tgttcttctg tttaatggtg gagttacctt 850
aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900
agcgaaagat aatgtgtgtg gctgggtattg gacttgttgt attattcttc 950
agttggatgc tctctatttt tagatctaaa tatcatggct acccatacag 1000
ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050
ggaaattgaa aaacgaaaat cgtgtgtgtt tgaaaagaag aatgcaactt 1100
gtatatattt tattacctct ttttttcaag tgatttaa atgttaatcat 1150
ttaaccaaag aagatgtgta gtgccttaac aagcaatcct ctgtcaaaat 1200
ctgaggtatt tgaaaataat tatcctctta accttctctt cccagtgaac 1250
tttatggaac atttaattta gtacaattaa gtatattata aaaattgtaa 1300
aactactact ttgttttagt tagaacaag ctcaaaacta ctttagttaa 1350
cttggtcatc tgattttata ttgccttata caaagatggg gaaagtaagt 1400
cctgaccagg tgttcccaca tatgcctgtt acagataact acattaggaa 1450

ttcattctta gcttcttcat ctttgtgtgg atgtgtatac tttacgcatac 1500
 tttccttttg agtagagaaa ttatgtgtgt catgtggtct tctgaaaatg 1550
 gaacaccatt cttcagagca cacgtctagc cctcagcaag acagttgttt 1600
 ctctctctcc ttgcatattt cctactgcgc tccagcctga gtgatagagt 1650
 gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataatttct 1700
 gcttgagtat ggtgttaact accttgatt tagaaagatt tcagattcat 1750
 tccatctcct tagttttctt ttaaggtgac ccatctgtga taaaaatata 1800
 gcttagtgct aaaatcagtg taacttatac atggcctaaa atgtttctac 1850
 aaattagagt ttgtcactta ttccatttgt acctaagaga aaaataggct 1900
 cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950
 tcagcacttt gggaggccaa ggcaggcaga tcacgaggtc aggagttcga 2000
 gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050
 attagctggg tgtggtggca ggagcctgta atcccagcta cacaggaggc 2100
 tgaggcacga gaatcacttg aactcaggag atggagggtt cagtgagccg 2150
 agatcacgcc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200
 aaaaaaaaaa aaa 2213

<210> 130
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 130
 Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val
 1 5 10 15
 Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
 20 25 30
 Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
 35 40 45
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
 50 55 60
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
 65 70 75
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
 80 85 90
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
 95 100 105

Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp
 110 115 120
 Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser
 125 130 135
 Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg
 140 145 150
 Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln
 155 160 165
 Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val
 170 175 180
 Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu
 185 190 195
 Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met
 200 205 210
 Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys
 215 220 225
 Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
 230 235 240
 Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn
 245 250 255
 Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His
 260 265 270
 Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu
 275 280 285
 Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys
 290 295 300
 Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser
 305 310 315
 Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr
 320 325 330
 Ser Phe Leu Met Ser
 335

<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

<400> 131
 aagcaaccaa actgcaagct ttgggagttg ttcgctgtcc ctgccctgct 50
 ctgctaggga gagaacgcca gagggaggcg gctggcccgg cggcaggctc 100

tcagaaccgc taccggcgat gctactgctg tgggtgctcg tggctgcagc 150
 cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
 cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
 aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
 ctttatgaag acacgtggga cttcctttct gaatgcctac acaactctc 350
 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
 ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450
 atggatggat gtcattggaga ggcattggta ccgaacacag aaatttgga 500
 aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
 tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggt 600
 taatcttatt cgtaacagga ctaaagtcag agtgatggaa agggattggc 650
 agaatacaga caaagcagta aactgggtta gaaaggaagc aattaattac 700
 actgaaccat ttgttattta cttgggatta aatttaccac acccttacc 750
 ttcaccatct tctggagaaa attttggatc ttcaacattt cacacatctc 800
 tttattggct tgaaaaagtg tctcatgatg ccatcaaat cccaaagtgg 850
 tcacctttgt cagaaatgca cctgtagat tattactctt cttatacaaa 900
 aaactgcact ggaagattta caaaaaaaga aattaagaat attagagcat 950
 tttattatgc tatgtgtgct gagacagatg ccattgcttg tgaaattatt 1000
 ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050
 ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaatga 1100
 gcatgtacga ggctagtga catgttccgc ttttgatgat gggaccagga 1150
 attaaagccg gcctacaagt atcaaatgtg gtttctcttg tggatattta 1200
 ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagtg 1250
 gatactcttt gttgccgtta tcatcagaaa catttaagaa tgaacataaa 1300
 gtcaaaaacc tgcattccac ctggattctg agtgaattcc atggatgtaa 1350
 tgtgaatgcc tccacctaca tgcttcgaac taaccactgg aaatatatag 1400
 cctattcgga tggatgcatc atattgcctc aactctttga tctttcctcg 1450
 gatccagatg aattaacaaa tgttgctgta aaatttccag aaattactta 1500
 ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600
 ataggacaga attattcaaa cgttatagca aatcttaggt ggcaccaaga 1650
 ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700
 aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagtg 1750
 ttctagagat acatataaat atattacaag atcataatta tgtattttaa 1800
 atgaaacagt ttttaataatt accaagtttt ggccggggcac agtggctcac 1850
 acctgtaatc ccaggacttt gggaggctga ggaaagcaga tcacaaggtc 1900
 aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950
 aaatacaaaa attagctggg cgcggtggtg cacacctata gtctcagcta 2000
 ctcagaggct gaggcaggag gatcgcttga acccgggagg cagcagttgc 2050
 agtgagctga gattgcgcca ctgtactcca gcctggcaac agagtgagac 2100
 tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150
 tattttgtaa gaatgtagtg tattttaaga taaaatgcc aatgattataa 2200
 aatcacatat ttcaaaaat gggtattatt taggcctttg tacaatttct 2250
 aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300
 atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350
 taaaatagtt gtatgtgagc atttgatggt gaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2450
 aaaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132

<211> 536

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Leu	Trp	Val	Ser	Val	Val	Ala	Ala	Leu	Ala	Leu	Ala	15
1				5					10						
Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys	30
				20					25						
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg	45
				35					40						
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile	60
				50					55						
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr	75
				65					70						

Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly	80	85	90
Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu	95	100	105
Asp Pro Asn Tyr Thr Thr Trp Met Asp Val Met Glu Arg His Gly	110	115	120
Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His	125	130	135
His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala	140	145	150
Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg	155	160	165
Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr	170	175	180
Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr	185	190	195
Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr	200	205	210
Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His	215	220	225
Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys	230	235	240
Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr	245	250	255
Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys	260	265	270
Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu	275	280	285
Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu	290	295	300
Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly	305	310	315
Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr	320	325	330
Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile	335	340	345
Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile	350	355	360
Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn			

365										370					375				
Leu	Ser	Gly	Tyr	Ser	Leu	Leu	Pro	Leu	Ser	Ser	Ser	Glu	Thr	Phe	Lys				
				380					385						390				
Asn	Glu	His	Lys	Val	Lys	Asn	Leu	His	Pro	Pro	Trp	Ile	Leu	Ser					
				395					400					405					
Glu	Phe	His	Gly	Cys	Asn	Val	Asn	Ala	Ser	Thr	Tyr	Met	Leu	Arg					
				410					415					420					
Thr	Asn	His	Trp	Lys	Tyr	Ile	Ala	Tyr	Ser	Asp	Gly	Ala	Ser	Ile					
				425					430					435					
Leu	Pro	Gln	Leu	Phe	Asp	Leu	Ser	Ser	Asp	Pro	Asp	Glu	Leu	Thr					
				440					445					450					
Asn	Val	Ala	Val	Lys	Phe	Pro	Glu	Ile	Thr	Tyr	Ser	Leu	Asp	Gln					
				455					460					465					
Lys	Leu	His	Ser	Ile	Ile	Asn	Tyr	Pro	Lys	Val	Ser	Ala	Ser	Val					
				470					475					480					
His	Gln	Tyr	Asn	Lys	Glu	Gln	Phe	Ile	Lys	Trp	Lys	Gln	Ser	Ile					
				485					490					495					
Gly	Gln	Asn	Tyr	Ser	Asn	Val	Ile	Ala	Asn	Leu	Arg	Trp	His	Gln					
				500					505					510					
Asp	Trp	Gln	Lys	Glu	Pro	Arg	Lys	Tyr	Glu	Asn	Ala	Ile	Asp	Gln					
				515					520					525					
Trp	Leu	Lys	Thr	His	Met	Asn	Pro	Arg	Ala	Val									
				530					535										

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
 gagagaagtc agcctggcag agagactctg aaatgagggg ttagagggtgt 50
 tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100
 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150
 ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
 catcaccagc tgtgacatct atagcaccct tctgggcctg cccgctgaca 350
 tccaggctgc ccaggccatg atggtgacat ccagtgaat ctctccctg 400
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atccccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500
 ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatc 550
 ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600
 tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650
 ctggaatcat cctctgcttt tcctgctcat cccagagaaa tcgctccaac 700
 tactacgatg cctaccaagc ccaacctott gccacaagga gctctccaag 750
 gcctgggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800
 caggggtatgt gtgaagaacc aggggccaga gctgggggggt ggctgggtct 850
 gtgaaaaaca gtggacagca ccccgagggc cacagggtgag ggacactacc 900
 actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950
 ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000
 attgccaagg atgctcgcca tgccagcctt tctgttttcc tcaccttget 1050
 gctccccctgc cctaagtccc caaccctcaa cttgaaaccc cattccctta 1100
 agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150
 ccccaaacc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200
 cctctctctt ggctgaggtt ggctcttagc tcattgctgg ggatgggaag 1250
 gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300
 cctccaaaga aactgattgg ccctggaacc tccatcccac tcttgttatg 1350
 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400
 tacggtatcc agggaaacaga aagcaggatg caggatggga ggacaggaag 1450
 gcagcctggg acatttaaaa aaata 1475

<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu
1				5					10					15

Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp
				20					25					30

Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly
				35					40					45

Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50										55					60				
Ile	Thr	Gln	Cys	Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala					
				65					70					75					
Asp	Ile	Gln	Ala	Ala	Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile					
				80					85					90					
Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr					
				95					100					105					
Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala	Val	Ala					
				110					115					120					
Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile	Pro					
				125					130					135					
Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro					
				140					145					150					
Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr					
				155					160					165					
Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile					
				170					175					180					
Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr					
				185					190					195					
Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg					
				200					205					210					
Pro	Gly	Gln	Pro	Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr	Ser					
				215					220					225					
Leu	Thr	Gly	Tyr	Val															
				230															

<210> 135
 <211> 610
 <212> DNA
 <213> Homo sapiens

<400> 135
 gcactgctgc tgtcccatca gctgctctga agctccatgg tgcccagaat 50
 cttegcctct gcttatgtgt cagtctgtct cctcctcttg tgtccaaggg 100
 aagtcacgcg tcccgcgtggc tcagaacctat ggctgtgcca gccggcaccc 150
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
 cgccatcgctg tccctgagcg agaccgcgcca atgtggtccc ccctgcacct 250
 tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcacaac 300
 gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaaat gtgaaagcag aagacgtttt ccctgagaag 400
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaattttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
 1 5 10 15
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
 ctccactgca accacccaga gccatggctc cccgaggctg catcgtagct 50
 gtcttttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100
 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtgcc cctggacctt catggtgaag ctgataaacc 300
 agaactgcga ctcagcccg acctcggatg acaggctttg tcgcagtgtc 350
 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
 gacctgtctg agggccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550
 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600
 ggactctgaa ccctctgat gaccctatg gccaacatca acccggcacc 650
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
 tatgtacttt ataatgaaa a 771

<210> 138

<211> 110

<212> PRT

<213> Homo sapiens.

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys
1				5					10					15

Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met
			20						25					30

Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp
			35						40					45

Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val
			50						55					60

Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg
			65						70					75

Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu
			80						85					90

Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu
			95						100					105

Cys	Arg	Ser	Val	Ser
			110	

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

gggggcgggg gcctggagca cggcgctggg gccgcccga gcgctcactc 50
 gctcgactc agtcgcggga ggcttccccg cgcggccgc gtcccggccg 100
 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200
 tctcttcctg gctgcgtccc taggtccggg ggcagccttc aaggtcgcca 250
 cgccgtattc cctgtatgtc tgtcccgagg ggcagaacgt caccctcacc 300
 tgcaggctct tgggccctgt ggacaaaggg cagcatgtga ccttctacaa 350
 gacgtggtac cgcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400
 ggcccatccg caacctcag ttccaggacc ttcacctgca ccatggaggc 450
 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500
 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
 ccctgctgga tagcggcctc tactgtctgc tgggtggtgga gatcaggcac 600
 caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650
 aggcaaagat gcaccatcca actgtgtggt gtacccatcc tcctcccagg 700
 atagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcatcgta 750
 ggaatcctct gctccccct catcctgtct ctggtctaca agcaaaggca 800
 ggcagcctcc aaccgccgtg ccaggagct ggtgcggatg gacagcaaca 850
 ttcaagggat tgaaaacccc ggctttgaag cctcaccacc tgcccagggg 900
 atacccgagg ccaaagtcag gcacccctg tcctatgtgg ccagcgga 950
 gccttctgag tctgggcggc atctgcttcc ggagcccagc accccctgt 1000
 ctctccagg ccccgagac gtcttcttcc catccctgga ccctgtccct 1050
 gactctcaa actttgagg catctagccc agctggggga cagtgggctg 1100
 ttgtggctgg gtctggggca ggtgcatttg agccagggt ggctctgtga 1150
 gtggcctcct tggcctcggc cctggttccc tccctcctgc tctgggctca 1200
 gatactgtga catcccagaa gccagcccc tcaaccctc tggatgctac 1250
 atggggatgc tggacggctc agccctgtt ccaaggattt tggggtgctg 1300
 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450

tgggccaccc tcccaggcac cagacacagg gcacggtgga gagacttctc 1500
 ccccgtaggc gccttggtc ccccgttttg cccgaggctg ctcttctgtc 1550
 agacttctc tttgtaccac agtggctctg gggccaggcc tgcctgcca 1600
 ctggccatcg ccaccttccc cagctgcctc ctaccagcag tttctctgaa 1650
 gatctgtcaa caggttaagt caatctgggg cttccactgc ctgcattcca 1700
 gtccccagag cttggtgggc ccgaaacggg aagtacatat tggggcatgg 1750
 tggcctccgt gagcaaattg tgtcttgggc aatctgaggc caggacagat 1800
 gttgcccac ccactggaga tgggtgctgag ggaggtgggt ggggccttct 1850
 gggaaggatga gtggagaggg gcacctgccc cccgccctcc ccatccccta 1900
 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
 ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly	1	5	10	15
Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val	20	25	30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	35	40	45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	50	55	60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	65	70	75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	80	85	90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	95	100	105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	110	115	120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	125	130	135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu				

140										145					150				
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu					
				155					160					165					
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val					
				170					175					180					
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala					
				185					190					195					
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu					
				200					205					210					
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg					
				215					220					225					
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile					
				230					235					240					
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro					
				245					250					255					
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln					
				260					265					270					
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro					
				275					280					285					
Leu	Ser	Pro	Pro	Gly	Pro	Gly	Asp	Val	Phe	Phe	Pro	Ser	Leu	Asp					
				290					295					300					
Pro	Val	Pro	Asp	Ser	Pro	Asn	Phe	Glu	Val	Ile									
				305					310										

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
 cccacgcgtc cgcgccctctc ccttctgctg gaccttcctt cgtctctcca 50
 tctctccctc ctttccccgc gttctcttcc cacctttctc ttcttccac 100
 cttagacctc ccttctgccc ctcccttctc gccaccgct gcttctggtc 150
 ccttctccga ccccgctcta gcagcagacc tcttgggggc tgtgggttga 200
 tctgtggccc ctgtgctccc gtgtcctttt cgtctccctt cctcccgact 250
 ccgctccccg accagcggcc tgacctggg gaaaggatgg ttcccagagt 300
 gagggctctc tctccttgc tgggactcgc gctgctctgg ttcccctgg 350
 actcccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400
 agatactccc ccggcgagag ctggcaccct tacttggagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttggt 500
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600
ggccccacca aagtcctgcc agcacaacgg gaccatgtac caacacggag 650
agatcttcag tgcccatgag ctgttcccct cccgcctgcc caaccagtgt 700
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
ccccgaacca ggctgccag caccctccc actgccagac tctgctgcc 800
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
cagtcgtcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900
tgggagaaag agaggcccgg gcacccagc cccactggc ctcagcgccc 950
ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
cggaagacg tactccacg gggaggtgtg gcaccgggc ttccgtgctt 1100
tcggcccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150
tgccagcgtg tgacctgtcc caccgagtac cctgccgtc accccgagaa 1200
agtggctggg aagtgtgca agatttgccc agaggacaaa gcagaccctg 1250
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
ctcgtccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350
cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400
taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450
ccacacagcc agaattctcc acttgactca gatcaagaaa gtcaggaagc 1500
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600
ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142

<211> 451

<212> PRT

<213> Homo sapiens

<400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala		1	5	10	15
Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp		20	25	30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser		35	40	45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg		50	55	60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His		65	70	75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln		80	85	90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg		95	100	105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His		110	115	120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro		125	130	135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys		140	145	150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro		155	160	165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu		170	175	180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg		185	190	195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly		200	205	210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe		215	220	225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val		230	235	240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly		245	250	255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg		260	265	270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly		275	280	285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys					

290										295					300				
Arg	His	Pro	Glu	Lys	Val	Ala	Gly	Lys	Cys	Cys	Lys	Ile	Cys	Pro					
				305					310					315					
Glu	Asp	Lys	Ala	Asp	Pro	Gly	His	Ser	Glu	Ile	Ser	Ser	Thr	Arg					
				320					325					330					
Cys	Pro	Lys	Ala	Pro	Gly	Arg	Val	Leu	Val	His	Thr	Ser	Val	Ser					
				335					340					345					
Pro	Ser	Pro	Asp	Asn	Leu	Arg	Arg	Phe	Ala	Leu	Glu	His	Glu	Ala					
				350					355					360					
Ser	Asp	Leu	Val	Glu	Ile	Tyr	Leu	Trp	Lys	Leu	Val	Lys	Asp	Glu					
				365					370					375					
Glu	Thr	Glu	Ala	Gln	Arg	Gly	Glu	Val	Pro	Gly	Pro	Arg	Pro	His					
				380					385					390					
Ser	Gln	Asn	Leu	Pro	Leu	Asp	Ser	Asp	Gln	Glu	Ser	Gln	Glu	Ala					
				395					400					405					
Arg	Leu	Pro	Glu	Arg	Gly	Thr	Ala	Leu	Pro	Thr	Ala	Arg	Trp	Pro					
				410					415					420					
Pro	Arg	Arg	Ser	Leu	Glu	Arg	Leu	Pro	Ser	Pro	Asp	Pro	Gly	Ala					
				425					430					435					
Glu	Gly	His	Gly	Gln	Ser	Arg	Gln	Ser	Asp	Gln	Asp	Ile	Thr	Lys					
				440					445					450					

Thr

<210> 143

<211> 693

<212> DNA

<213> Homo sapiens

<400> 143

ctagcctgcg ccaaggggta gtgagaccgc gcggcaacag cttgcggctg 50

cggggagctc ccgtgggcgc tccgctggct gtgcaggcgg ccatggattc 100

cttgcggaat atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150

tgggctacgc gtcctcgtt atcgtgaccc cgggagagcg gcggaagcag 200

gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250

ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300

cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350

ggcgccagcg ggaggtcacc gtgagaccgc acttgctcc gtgggcgccg 400

gaccttggct tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggctcct 500
 gtgagctgcc gtccgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 ttttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
 1 5 10 15
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
 caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcgggc 50
 ttgaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100
 caggctgccca tggggcccag caccctctc ctcactttgt tccttttgtc 150
 atggtcggga cccctccaag gacagcagca ccaccttggt gagtacctgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcaactcaga actgaggccg 350
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagaccacaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
tggaggccct gggaccaaag gcaagggaaag aaggaatgag aagtacgata 500
tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600
gcaaacagag aagatctacg tgtagatgg gacacagaat gacacagcct 650
ttgtcttccc aaggctgctg gacttcaccc ttgccatggc tgcccggaaa 700
gcttcccagag tccgggtgcc cttcccctgg gtaggcacag ggcagctggt 750
atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800
gagggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850
aaccgaacag tgggtggacag ctacgtattc ccagcagagg ggctgatccc 900
cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950
aaggctcttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000
ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050
accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100
tctatgtcgt ctataacacc cgtcctgcc gtcggggccg catccagtgc 1150
tcctttgatg ccagcggcac cctgacctt gaacgggcag cactccctta 1200
ttttccccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250
aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300
gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350
catctttctc actcccatc atttatatta tatccccact aaatttcttg 1400
ttcctcattc ttcaaagtgt ggccagtgt ggctcaaact ctctatattt 1450
ttagccaatg gcaatcaaat tctttcagct cctttgtttc atacggaact 1500
ccagatcctg agtaatcctt ttagagcccg aagagtcaaa acctcaatg 1550
ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc 1600
cccagacca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650
agcagtgttc ttcccctcag agtgacttgg ggaggagaa ataggaggag 1700
acgtccagct ctgtcctctc ttcctcactc ctcccttcag tgtcctgagg 1750
aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800
gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146
<211> 406
<212> PRT
<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
1				5					10					15
Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
			20					25						30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
			35					40						45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
			50					55						60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
			65					70						75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
			80						85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
			95						100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
			110						115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
			125						130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
			140						145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
			155						160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
			170						175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
			185						190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
			200						205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
			215						220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
			230						235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
			245						250					255

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	260	265	270
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	275	280	285
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	290	295	300
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	305	310	315
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	320	325	330
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	335	340	345
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	350	355	360
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	365	370	375
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	380	385	390
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	395	400	405

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
 gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgcct 50
 ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100
 gttctctct tctctctaata ccatccgtca cctctctctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttgggttctga gtctctctcaa gctgggatca gggcagtggc aggtgtttgg 250
 gccagacaag cctgtccagg ccttgggtggg ggaggacgca gcattctcct 300
 gtttctctgtc tctaagacc aatgcagagg ccatggaagt gcggttcttc 350
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
 attctattgc ggagggggcgc atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650
 tcgggctggt tccccggcc cacagcgaag tggaaaggtc cacaaggaca 700
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggctgtttg 750
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800
 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtagagat 850
 aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900
 tgggaatact ctgctgtggc ctattttttg gcattgttgg actgaagatt 950
 ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050
 tgactctgga tccagagacg gctcacccga agctctgcgt ttctgatctg 1100
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcagggg 1200
 aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga 1250
 gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
 cattaaatcc ccgttttata agcgtcttcc ccaggacccc acctacaaaa 1400
 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450
 aaatgaccag tcccttattt ataccctgac atgtcggttt gaaggcttat 1500
 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaaactccc 1550
 atagtcatct gccagtcac ccaggaatca gagaaagagg cctcttggca 1600
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650
 caaccacgcc ctctctcccc aggggtgaaa tgtaggatga atcacatccc 1700
 acattcttct ttagggatat taaggctctct ctcccagatc caaagtcccg 1750
 cagcagcccg ccaagggtgc ttccagatga agggggactg gcctgtccac 1800
 atgggagtca ggtgtcatgg ctgccctgag ctgggagggg agaaggctga 1850
 cattacattt agtttctct cactccatct ggctaagtga tcttgaaata 1900
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
 acagagtgta tcctaattggt ttgttcatta tattacactt tcagtaaaaa 2050
 aa 2052

<210> 148
 <211> 500
 <212> PRT
 <213> Homo sapiens

<400> 148
 Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly
 1 5 10 15
 Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala
 20 25 30
 Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys
 35 40 45
 Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe
 50 55 60
 Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe
 65 70 75
 Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp
 80 85 90
 Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr
 95 100 105
 Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser
 110 115 120
 Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly
 125 130 135
 Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile
 140 145 150
 Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala
 155 160 165
 Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg
 170 175 180
 Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu
 185 190 195
 Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His
 200 205 210
 Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp
 215 220 225
 Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

230										235					240				
Gly	Ile	Leu	Cys	Cys	Gly	Leu	Phe	Phe		Gly	Ile	Val	Gly	Leu	Lys				
				245						250					255				
Ile	Phe	Phe	Ser	Lys	Phe	Gln	Trp	Lys		Ile	Gln	Ala	Glu	Leu	Asp				
				260						265					270				
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu		Leu	Arg	Asp	Ala	Arg	Lys				
				275						280					285				
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro		Glu	Thr	Ala	His	Pro	Lys				
				290						295					300				
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val		Thr	His	Arg	Lys	Ala	Pro				
				305						310					315				
Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg		Phe	Thr	Arg	Lys	Ser	Val				
				320						325					330				
Val	Ala	Ser	Gln	Ser	Phe	Gln	Ala	Gly		Lys	His	Tyr	Trp	Glu	Val				
				335						340					345				
Asp	Gly	Gly	His	Asn	Lys	Arg	Trp	Arg		Val	Gly	Val	Cys	Arg	Asp				
				350						355					360				
Asp	Val	Asp	Arg	Arg	Lys	Glu	Tyr	Val		Thr	Leu	Ser	Pro	Asp	His				
				365						370					375				
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Asn	Gly		Glu	His	Leu	Tyr	Phe	Thr				
				380						385					390				
Leu	Asn	Pro	Arg	Phe	Ile	Ser	Val	Phe		Pro	Arg	Thr	Pro	Pro	Thr				
				395						400					405				
Lys	Ile	Gly	Val	Phe	Leu	Asp	Tyr	Glu		Cys	Gly	Thr	Ile	Ser	Phe				
				410						415					420				
Phe	Asn	Ile	Asn	Asp	Gln	Ser	Leu	Ile		Tyr	Thr	Leu	Thr	Cys	Arg				
				425						430					435				
Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile		Glu	Tyr	Pro	Ser	Tyr	Asn				
				440						445					450				
Glu	Gln	Asn	Gly	Thr	Pro	Ile	Val	Ile		Cys	Pro	Val	Thr	Gln	Glu				
				455						460					465				
Ser	Glu	Lys	Glu	Ala	Ser	Trp	Gln	Arg		Ala	Ser	Ala	Ile	Pro	Glu				
				470						475					480				
Thr	Ser	Asn	Ser	Glu	Ser	Ser	Ser	Gln		Ala	Thr	Thr	Pro	Phe	Leu				
				485						490					495				
Pro	Arg	Gly	Glu	Met															
				500															

<210> 149

<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcc cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcggcg gcggttgcg aggcttcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgccct gttgtgctgc gccgccgcg ccgccgccgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cggtggcggc ggggccgcg ggcaggtgga 250
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300
gggcgacggc tcccacggcc caggccccga ggaccgggc cccgcgcgcc 350
accgtccacc gacccctggc tgcgacttct ccagcccagt ccccgagac 400

caccctcttt tgggagactg ctggaccctc ttccaccacc tttcaggcgc 450
cgctcgggcc ctcgccgacc acccctccgg cggcggaacg cacttcgacc 500
acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550
tggcccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600
ctccccggac ccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650
ctccccaccc cacctgccac cgaggccccc tcttcgcctc ctccagagta 700
tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750
agaccacagg gcagtgtgag tgtcggccag gttatcaggg gcttcactgt 800
gaaacctgca aagagggctt ttacctaaat tacacttctg ggctctgtca 850
gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900
aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaacaa 950
aaaaggctgc tactctcaag gaccatactg gtttaaacia aggaggatga 1000
gggtcataga tttaaaaaat attttatata cttttattct cttactttat 1050
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100
tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150
atttcatggg aaaaaattat tgaagaataa atctgctttc tggaagggct 1200
ttcaggcatg aaacctgcta ggaggttttag aaatgttctt atgtttatta 1250
atataccatt ggagtttgag gaaatttgtt gtttggttta tttttctctc 1300
taatcaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350
ggtaccctaa tttatttaac tagtggttaag tagactgggt ttactctatt 1400
taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450
aactattatg ttatttgag gtaatttaat ctagtggaat aatgtactgt 1500
tatctaagca tttgccttgt actgcactga aagtaattat tctttgacct 1550
tatgtgaggc acttggcttt ttgtggaccc caagtcaaaa aactgaagag 1600
acagtattaa ataataaaaa aaataatgac aggttatact cagtgttaacc 1650
tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700
agtaatttcc tttcactgag cttgtttctt ctcaagggtt ttgtgaagat 1750
taaataagtt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800
ctggtttgtt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgttttaaga acttttagct ccttgacaaa gaagtgcctt atactttagc 1900
 actaaatatt ttaaagctt tataaatgat attatactgt tatggaatat 1950
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000
 ctcacgcctg taatcctagc actttgggag gccaaaggcgg gtggatcact 2050
 tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgctct 2100
 ctactaaaaa tacaacaaa ttagctgggc gtggtggcac acacctgtag 2150
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200
 tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250
 agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153
 <211> 258
 <212> PRT
 <213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys	1	5	10	15
Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn	20	25	30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro	35	40	45	
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala	50	55	60	
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala	65	70	75	
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro	80	85	90	
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr	95	100	105	
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala	110	115	120	
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro	125	130	135	
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val	140	145	150	
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro	155	160	165	
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro				

	170	175	180
Ala Thr Glu Ala	Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys	Asn
	185	190	195
Cys Ser Val Val	Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln	Thr
	200	205	210
Thr Gly Gln Cys	Glu Cys Arg Pro Gly	Tyr Gln Gly Leu His	Cys
	215	220	225
Glu Thr Cys Lys	Glu Gly Phe Tyr Leu	Asn Tyr Thr Ser Gly	Leu
	230	235	240
Cys Gln Pro Cys	Asp Cys Ser Pro His	Gly Ala Leu Ser Ile	Pro
	245	250	255

Cys Asn Arg

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 154
 aactgctctg tgggtggaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 155
 cagtcacatg gctgacagac ccac 24

<210> 156
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-38
 <223> Synthetic construct.

<400> 156
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
 tgccggcgag ttagacctg ggaggatggg cggcctgctg ctggctgctt 50
 ttctggcttt ggtctcggtg cccaggggcc aggccgtgtg gttgggaaga 100
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150
 ccgggaaaag ggctttgcca tggagaagga catgaagaac gtcgtggggg 200
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
 cacgggctgg gaggggtgtg ccagagtgtc atggacctga taaagcgaaa 300
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
 tgctggccac caacttcaga gactatgcc aatctttcac tcagctggag 400
 ttccggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gagggcatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttctctgt acagtagcag gccagctgc agaaggacct cacctgtgct 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600
 gggctctgtg acctcgcca gtgtccacc acctcgctca gcggctcccg 650
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159
 <211> 1665
 <212> DNA
 <213> Homo sapiens

<400> 159
 aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50
 gctgctgctg cccctgctct gggggaggga gagggcgga ggacagacaa 100
 gtaaactgct gacgatgcag agttccgtga cggtcagga aggcctgtgt 150
 gtccatgtgc cctgctcctt ctctacccc tcgcatggct ggatttacc 200
 tggcccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250
 aggatgtccc agtggccaca aacaacccag ctcgggcagt gtgggaggag 300
 actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
 cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400
 gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
 gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
 cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
 gtgagcaggg gacaccccct atgatctcct ggataggac ctccgtgtcc 600
 cccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650
 gcccaggac catggcacca gcctcacctg tcaggtgacc ttccctggg 700
 ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctaccgcct 750
 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
 cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
 tggctctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900
 ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg 950

ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
 gcagagctca gaacctctc ggctctcagc aggtctacct gaacgtctcc 1050
 ctgcagagca aagccacatc aggagtgact caggggggtgg tcgggggagc 1100
 tggagccaca gccctggtct tctgtcctt ctgcgtcatc ttcgtttag 1150
 tgaggctctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
 acgggcatag aggatgcaaa cgctgtcagg gggttcagcct ctcagggggc 1250
 cctgactgaa ccttgggcag aagacagtcc cccagaccag cctccccag 1300
 cttctgcccg ctctcagtg ggggaaggag agctccagta tgcattccctc 1350
 agcttcacaga tggatgaagc ttgggactcg cggggacagg agggcactga 1400
 caccgagtag tcggagatca agatccacag atgagaaact gcagagactc 1450
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataacact 1550
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600
 tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650
 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala	1	5	10	15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr	20	25	30	
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr	35	40	45	
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr	50	55	60	
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala	65	70	75	
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg	80	85	90	
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser	95	100	105	
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg				

110										115					120				
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu					
				125					130					135					
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile					
				140					145					150					
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser					
				155					160					165					
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp					
				170					175					180					
Ile	Gly	Thr	Ser	Val	Ser	Pro	Leu	Asp	Pro	Ser	Thr	Thr	Arg	Ser					
				185					190					195					
Ser	Val	Leu	Thr	Leu	Ile	Pro	Gln	Pro	Gln	Asp	His	Gly	Thr	Ser					
				200					205					210					
Leu	Thr	Cys	Gln	Val	Thr	Phe	Pro	Gly	Ala	Ser	Val	Thr	Thr	Asn					
				215					220					225					
Lys	Thr	Val	His	Leu	Asn	Val	Ser	Tyr	Pro	Pro	Gln	Asn	Leu	Thr					
				230					235					240					
Met	Thr	Val	Phe	Gln	Gly	Asp	Gly	Thr	Val	Ser	Thr	Val	Leu	Gly					
				245					250					255					
Asn	Gly	Ser	Ser	Leu	Ser	Leu	Pro	Glu	Gly	Gln	Ser	Leu	Arg	Leu					
				260					265					270					
Val	Cys	Ala	Val	Asp	Ala	Val	Asp	Ser	Asn	Pro	Pro	Ala	Arg	Leu					
				275					280					285					
Ser	Leu	Ser	Trp	Arg	Gly	Leu	Thr	Leu	Cys	Pro	Ser	Gln	Pro	Ser					
				290					295					300					
Asn	Pro	Gly	Val	Leu	Glu	Leu	Pro	Trp	Val	His	Leu	Arg	Asp	Ala					
				305					310					315					
Ala	Glu	Phe	Thr	Cys	Arg	Ala	Gln	Asn	Pro	Leu	Gly	Ser	Gln	Gln					
				320					325					330					
Val	Tyr	Leu	Asn	Val	Ser	Leu	Gln	Ser	Lys	Ala	Thr	Ser	Gly	Val					
				335					340					345					
Thr	Gln	Gly	Val	Val	Gly	Gly	Ala	Gly	Ala	Thr	Ala	Leu	Val	Phe					
				350					355					360					
Leu	Ser	Phe	Cys	Val	Ile	Phe	Val	Val	Val	Arg	Ser	Cys	Arg	Lys					
				365					370					375					
Lys	Ser	Ala	Arg	Pro	Ala	Ala	Gly	Val	Gly	Asp	Thr	Gly	Ile	Glu					
				380					385					390					
Asp	Ala	Asn	Ala	Val	Arg	Gly	Ser	Ala	Ser	Gln	Gly	Pro	Leu	Thr					
				395					400					405					

Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagt 200
 aaggtgacag ccctggggcg tgggaagttg gaagccacgt tcaccttcac 250
 gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcccc ggagggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccga 550
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctacc tccagccatg acccttcct 650
 gctccacccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20										25					30				
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg					
				35					40					45					
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly					
				50					55					60					
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile					
				65					70					75					
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr					
				80					85					90					
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro					
				95					100					105					
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly					
				110					115					120					
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr					
				125					130					135					
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys					
				140					145					150					
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser					
				155					160					165					
Cys	Val	Pro	Glu	His															
				170															

<210> 163

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 163

ggagatgaag accctgttcc tg 22

<210> 164

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 164

ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gcctagtgtt cggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
caggacctg gtacgtgaag gccatgggtg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccttca ccctggagga ggaggatatc acagggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcatcggg 50
 cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100
 aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
 gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200
 ccagccctgg caggcagccc tggtcgagaa gacgcggcta ctctgtgggg 250
 cgacgctcat cgtccccaga tggctcctga cagcagccca ctgcctcaag 300
 ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
 ctgtgagcag acccggacag cactgagtc cttccccac cccggttca 400
 acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
 atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500
 ctcacgtgtg gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
 gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600
 atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
 cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
 gccaggggta ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
 attatctcct gggggccagga tccgtgtgcg atcaccgaa agcctggtgt 800
 ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850
 acaattagac tggaccacc caccacagcc catcaccctc catttccact 900
 tgggtgtttg ttctgttca ctctgttaat aagaaacct aagccaagac 950
 cctctacgaa cattctttg gcctcctgga ctacaggaga tgctgtcact 1000
 taataatcaa cctgggggtc gaaatcagtg agacctggat tcaaattctg 1050
 ccttgaaata ttgtgactct gggaatgaca acacctggtt tgttctctgt 1100
 tgtatcccca gccccaaga cagctcctgg ccatatatca aggtttcaat 1150
 aaatatattgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
 aaaa 1204

<210> 170

<211> 250

<212> PRT

<213> Homo sapiens

<400> 170

Met	Arg	Ile	Leu	Gln	Leu	Ile	Leu	Leu	Ala	Leu	Ala	Thr	Gly	Leu
1					5				10					15

Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro	20	25	30
His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu	35	40	45
Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala	50	55	60
Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His	65	70	75
Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr	80	85	90
Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys	95	100	105
Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val	110	115	120
Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys	125	130	135
Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr	140	145	150
Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn	155	160	165
Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly	170	175	180
Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly	185	190	195
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn	200	205	210
Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala	215	220	225
Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val	230	235	240
Asp Trp Ile Gln Glu Thr Met Lys Asn Asn	245	250	

<210> 171
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 171
ggctgcggga ctggaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgtagaca ccaggctttc ggggtg 25

<210> 176
<211> 18
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaag atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttggt cttgggtgtg ggcaagtc 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt ttgagattg aactttatgc 450
 tgtgacaaaa ggaccacgga gcattgagac atttaaacia atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
 tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650
 ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
 atttctactt ttttttttta gctatttact gtactttatg tataaaacia 750
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctggt 850
 ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 aaaaaaa 907

<210> 180
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
 1 5 10 15
 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
 20 25 30
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
 35 40 45
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
 50 55 60
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
 65 70 75
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
 80 85 90
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
 95 100 105
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
 110 115 120
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
 125 130 135
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
 140 145 150

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 181
 gtgttctgct ggagccgatg cc 22

<210> 182
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 182
 gacatggaca atgacagg 18

<210> 183
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 183
 cctttcagga tgtaggag 18

<210> 184
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 184
 gatgtctgcc accccaag 18

 <210> 185
 <211> 27
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

 <400> 185
 gcatcctgat atgacttgtc acgtggc 27

 <210> 186
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 186
 tacaagaggg aagaggagtt gcac 24

 <210> 187
 <211> 52
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-52
 <223> Synthetic construct.

 <400> 187
 gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

 cc 52

 <210> 188
 <211> 573
 <212> DNA
 <213> Homo sapiens

 <400> 188
 cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50

 ctctttggag ctgtgactca gaaaacaaaa acttctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150
 atacttctgg atctgggcag aaactattca cattccccctt ggagacatgt 200
 aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250
 aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
 atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
 ttcttgtttc atttcgcgac tgcctctca gtgtttcctg ggatcccctc 550
 ccaaataaag tacttatatt ctc 573

<210> 189
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 189
 Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
 1 5 10 15
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
 20 25 30
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
 35 40 45
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
 50 55 60
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
 65 70

<210> 190
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 190
 agggaaccatt gcttcttcca ggcc 24

<210> 191
 <211> 24
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggtc atcccccttgg tgaccttcaa agagaagcag agagggcaga 50
ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100
gacttttgaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc cttattgacc acagggtgggt cctcacagcg 300
gctcactgca gcggcagcag gtactgggtg cgcctggggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550
gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600
tgctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
cgggagaatc acgagcaaca tgggtgtgtgc aggcggcgtc ccggggcagg 700
atgcctgcca ggggtgattct gggggccccc tgggtgtgtg gggagtccct 750
caaggctctg tgcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850
 tcatgaggaa caactgacct gtttcctcca cctccacccc cacccttaa 900
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950
 ccctagctcc actcttggtg gcctgggaac ttcttggaac tttaactcct 1000
 gccagccctt ctaagacca cgagcggggt gagagaagtg tgcaatagtc 1050
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 194
 Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser
 1 5 10 15
 Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
 20 25 30
 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
 35 40 45
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
 50 55 60
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
 65 70 75
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
 80 85 90
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
 95 100 105
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
 110 115 120
 Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr
 125 130 135
 Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His
 140 145 150
 Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser
 155 160 165
 Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile
 170 175 180
 Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala
 185 190 195
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
 gcggccacac gcagctagcc ggagcccgga ccaggcgcct gtgcctcctc 50
 ctcgtccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150
 ggcttgctca aagccccgca ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccacac ctggagatga agaagatgat ctgagagggt acaggagggg 400
 tcagtacac tatatcctac cgagactttg tgaacatgat gctggggaaa 450
 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
 tgccctgagg acccgctg gactccccag ccttcccacc ccatacctcc 600
 ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650
 tttgtttggt cattgagggt ttgtttgtgt tttcatcaat gtctttgtaa 700
 agcaciaaatt atctgcctta aaggggctct gggtcgggga atcctgagcc 750
 ttgggtcccc tcctctctt cttccctcct tccccgctcc ctgtgcagaa 800
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcaggagg 850
 cttccagcct gtgttcccct cacttgaggg aaccagcact ctccatcctt 900
 tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950
 gacccaggc cactctgaga agaccttga gtagggacaa ggctgcaggg 1000
 cctctttcgg gtttccttgg acagtgccat ggttccagtg ctctggtgtc 1050

acccaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100
 attccacacc tcttctcatc ctcagtgatg tgaaggtggg aaggaaagga 1150
 gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200
 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250
 tactgtccct tactggggca gcagagggct tcggaggcag aagtgaggcc 1300
 tggggtttgg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450
 tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 196
 Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe
 1 5 10 15
 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
 20 25 30
 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
 35 40 45
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
 50 55 60
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
 65 70 75
 Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
 80 85 90
 Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
 95 100 105
 Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
 110 115 120
 Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
 125 130 135
 Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
 140 145 150

<210> 197
 <211> 4842
 <212> DNA
 <213> Homo sapiens

<400> 197

cgcgctcccc gcgcgcctcc tcgggctcca cgcgtcttgc cccgcagagg 50
cagcctcctc caggagcggg gccctgcaca ccatggcccc cgggtgggca 100
ggggtcggcg ccgccgtgcg cgcgcgcctg gcgctggcct tggcgctggc 150
gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200
gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttcct 250
cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300
caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350
tgcatctgga agacaaccag gtcagcgtca tcgagagagg cgccttcag 400
gacctgaagc agctagagcg actgcgcctg aacaagaata agctgcaagt 450
ccttcagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500
tgagtgaaaa ccagatccag gggatcccga ggaaggcgtt ccgcggcatc 550
accgatgtga agaacctgca actggacaac aaccacatca gctgcattga 600
agatggagcc ttccgagcgc tgcgcgattt ggagatcctt accctcaaca 650
acaacaacat cagtcgcac ctggtcacca gcttcaacca catgccgaag 700
atccgaactc tgcgcctcca ctccaaccac ctctactgcg actgccacct 750
ggcctggctc tcggattggc tgcgacagcg acggacagtt ggccagttca 800
cactctgcat ggctcctgtg catttgaggg gcttcaacgt ggcggtatgtg 850
cagaagaagg agtacgtgtg ccagccccc cactcggagc ccccatcctg 900
caatgccaac tccatctcct gcccttcgcc ctgcacgtgc agcaataaca 950
tcgtggactg tcgaggaaag ggcttgatgg agattcctgc caacttgccg 1000
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 1050
tgcaggagcc ttcacccagt acaagaaact gaagcgaata gacatcagca 1100
agaatcagat atcggatatt gctccagatg ccttcagggg cctgaaatca 1150
ctcacatcgc tggctctgta tgggaacaag atcaccgaga ttgccaaggg 1200
actgtttgat gggctgggtg ccctacagct gctcctcctc aatgccaaca 1250
agatcaactg cctgcgggtg aacacgtttc aggacctgca gaacctcaac 1300
ttgctctccc tgtatgacaa caagctgcag accatcagca aggggctctt 1350
cgccctctg cagtccatcc agacactcca cttagcccaa aaccttttg 1400
tgtgcgactg ccacttgaag tggctggccg actacctcca ggacaacccc 1450

atcgagacaa gcgggggccc ctgcagcagc ccgcgcccgc tcgccaacaa 1500
 gcgcatcagc cagatcaaga gcaagaagtt ccgctgctca ggctccgagg 1550
 attacgcag caggttcagc agcgagtgt tcatggacct cgtgtgcccc 1600
 gagaagtgtc gctgtgaggg cagcattgtg gactgctcca accagaagct 1650
 ggtccgcac ccaagccacc tcctgaata tgtcaccgac ctgcgactga 1700
 atgacaatga ggtatctgtt ctggaggcca ctggcatctt caagaagttg 1750
 cccaacctgc ggaaaataaa tctgagtaac aataagatca aggaggtgcg 1800
 agaggagct ttcgatggag cagccagcgt gcaggagctg atgctgacag 1850
 ggaaccagct ggagaccgtg caggggcgcg tggtccgtgg cctcagtggc 1900
 ctcaaacct tgatgctgag gagtaacttg atcagctgtg tgagtaatga 1950
 cacctttgcc ggctgagtt cggtagact gctgtccctc tatgacaatc 2000
 ggatcaccac catcaccctt ggggccttca ccacgcttgt ctccctgtcc 2050
 accataaacc tcctgtccaa ccccttcaac tgcaactgcc acctggcctg 2100
 gctcggaag tggttgagga agaggcgat cgtcagtggg aaccctaggt 2150
 gccagaagcc attttctctc aaggagattc ccatccagga tgtggccatc 2200
 caggacttca cctgtgatgg caacgaggag agtagctgcc agctgagccc 2250
 gcgctgcccg gagcagtga cctgtatgga gacagtgggt cgatgcagca 2300
 acaaggggct ccgcgcccct cccagaggca tgcccaagga tgtgaccgag 2350
 ctgtacctgg aaggaaacca cctaacagcc gtgcccagag agctgtccgc 2400
 cctccgacac ctgacgttta ttgacctgag caacaacagc atcagcatgc 2450
 tgaccaatta caccttcagt aacatgtctc acctctcac tctgatcctg 2500
 agctacaacc ggctgaggtg catccccgtc cagccttca acgggctgcg 2550
 gtccctgca gtgctaacc tccatggcaa tgacatttcc agcgttcctg 2600
 aaggctcctt caacgacctc acatctcttt cccatctggc gctgggaacc 2650
 aaccactcc actgtgactg cagtcttcgg tggctgtcgg agtgggtgaa 2700
 ggcggggtac aaggagcctg gcacgcccgc ctgcagtagc cctgagccca 2750
 tggctgacag gtcctgtctc accaccccaa cccaccgctt ccagtgcaa 2800
 gggccagtgg acatcaacat tgtggccaaa tgcaatgcct gcctctccag 2850
 cccgtgcaag aataacggga catgcaccca ggaccctgtg gagctgtacc 2900

gctgtgctg cccctacagc tacaagggca aggactgcac tgtgcccac 2950
aacacctgca tccagaaccc ctgtcagcat ggaggcacct gccacctgag 3000
tgacagccac aaggatgggt tcagctgctc ctgccctctg ggctttgagg 3050
ggcagcgggtg tgagatcaac ccagatgact gtgaggacaa cgactgcgaa 3100
aacaatgcca cctgcgtgga cgggatcaac aactacgtgt gtatctgtcc 3150
gcctaactac acaggtgagc tatgcgacga ggtgattgac cactgtgtgc 3200
ctgagctgaa cctctgtcag catgaggcca agtgcacccc cctggacaaa 3250
ggattcagct gcgagtgtgt ccctggctac agcgggaagc tctgtgagac 3300
agacaatgat gactgtgtgg ccacaaagt ccgccacggg gccagtgcg 3350
tggacacaat caatggctac acatgcacct gccccaggg cttcagtgga 3400
cccttctgtg aacaccccc acccatggtc ctactgcaga ccagcccatg 3450
cgaccagtac gagtgccaga acggggccca gtgcatcgtg gtgcagcagg 3500
agcccacctg ccgctgcca ccaggcttcg ccggcccag atgcgagaag 3550
ctcatcactg tcaacttctg gggcaaagac tcctacgtgg aactggcctc 3600
cgccaaggtc cgaccccagg ccaacatctc cctgcaggtg gccactgaca 3650
aggacaacgg catccttctc taaaaggag acaatgaccc cctggcactg 3700
gagctgtacc agggccacgt gcggctggtc tatgacagcc tgagttcccc 3750
tccaaccaca gtgtacagtg tggagacagt gaatgatggg cagtttcaca 3800
gtgtggagct ggtgacgcta aaccagaccc tgaacctagt agtggacaaa 3850
ggaactccaa agagcctggg gaagctccag aagcagccag cagtgggcat 3900
caacagcccc ctctaccttg gaggcacccc cacctccacc ggctctccg 3950
ccttgcgcca gggcacggac cggcctctag gcggcttcca cggatgcac 4000
catgaggtgc gcatcaacaa cgagctgcag gacttcaagg ccctcccacc 4050
acagtccttg ggggtgtcac caggctgcaa gtcctgcacc gtgtgcaagc 4100
acggcctgtg ccgctccgtg gagaaggaca gcgtggtgtg cgagtgccgc 4150
ccaggctgga ccggcccact ctgcgaccag gagggccggg acccctgcct 4200
cggccacaga tgccaccatg gaaaatgtgt ggcaactggg acctcataca 4250
tgtgcaagtg tgccgagggc tatggagggg acttgtgtga caacaagaat 4300
gactctgcca atgcctgctc agccttcaag tgtcaccatg ggcagtgcc 4350

catctcagac caaggggagc cctactgcct gtgccagccc ggcttttagcg 4400
 gcgagcactg ccaacaagag aatccgtgcc tgggacaagt agtccgagag 4450
 gtgatccgcc gccagaaagg ttatgcatca tgtgccacag cctccaaggt 4500
 gcccatcatg gaatgtcgtg ggggctgtgg gcccagtgcc tgccagccca 4550
 cccgcagcaa gcggcggaata tacgtcttcc agtgcacgga cggctcctcg 4600
 tttgtagaag aggtggagag acacttagag tgcggctgcc tcgctgttc 4650
 ctaagcccct gccgcctgct ctgccacctc tcggactcca gcttgatgga 4700
 gttgggacag ccatgtggga cccctggtg attcagcatg aaggaaatga 4750
 agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800
 aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198
 <211> 1523
 <212> PRT
 <213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg	1	5	10	15
Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro	20	25	30	
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val	35	40	45	
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro	50	55	60	
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg	65	70	75	
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu	80	85	90	
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe	95	100	105	
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys	110	115	120	
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu	125	130	135	
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg	140	145	150	
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp	155	160	165	

Asn Asn His Ile	Ser Cys Ile Glu Asp Gly	Ala Phe Arg Ala Leu
170	175	180
Arg Asp Leu Glu	Ile Leu Thr Leu Asn Asn Asn Ile Ser	Arg
185	190	195
Ile Leu Val Thr	Ser Phe Asn His Met Pro Lys Ile Arg Thr	Leu
200	205	210
Arg Leu His Ser	Asn His Leu Tyr Cys Asp Cys His Leu Ala	Trp
215	220	225
Leu Ser Asp Trp	Leu Arg Gln Arg Arg Thr Val Gly Gln Phe	Thr
230	235	240
Leu Cys Met Ala	Pro Val His Leu Arg Gly Phe Asn Val Ala	Asp
245	250	255
Val Gln Lys Lys	Glu Tyr Val Cys Pro Ala Pro His Ser Glu	Pro
260	265	270
Pro Ser Cys Asn	Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys	Thr
275	280	285
Cys Ser Asn Asn	Ile Val Asp Cys Arg Gly Lys Gly Leu Met	Glu
290	295	300
Ile Pro Ala Asn	Leu Pro Glu Gly Ile Val Glu Ile Arg Leu	Glu
305	310	315
Gln Asn Ser Ile	Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln	Tyr
320	325	330
Lys Lys Leu Lys	Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser	Asp
335	340	345
Ile Ala Pro Asp	Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser	Leu
350	355	360
Val Leu Tyr Gly	Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu	Phe
365	370	375
Asp Gly Leu Val	Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn	Lys
380	385	390
Ile Asn Cys Leu	Arg Val Asn Thr Phe Gln Asp Leu Gln Asn	Leu
395	400	405
Asn Leu Leu Ser	Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser	Lys
410	415	420
Gly Leu Phe Ala	Pro Leu Gln Ser Ile Gln Thr Leu His Leu	Ala
425	430	435
Gln Asn Pro Phe	Val Cys Asp Cys His Leu Lys Trp Leu Ala	Asp
440	445	450
Tyr Leu Gln Asp	Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys	Ser

455										460					465				
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser					
				470					475					480					
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe					
				485					490					495					
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg					
				500					505					510					
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg					
				515					520					525					
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn					
				530					535					540					
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys					
				545					550					555					
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys					
				560					565					570					
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu					
				575					580					585					
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val					
				590					595					600					
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn					
				605					610					615					
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser					
				620					625					630					
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr					
				635					640					645					
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu					
				650					655					660					
Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly					
				665					670					675					
Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys					
				680					685					690					
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala					
				695					700					705					
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln					
				710					715					720					
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val					
				725					730					735					
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met					
				740					745					750					

Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr	755	760	765
Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile	770	775	780
Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe	785	790	795
Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg	800	805	810
Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu	815	820	825
Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu	830	835	840
Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly	845	850	855
Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu	860	865	870
Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser	875	880	885
Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr	890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala	905	910	915
Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr	920	925	930
Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr	935	940	945
Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile	950	955	960
Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser	965	970	975
His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly	980	985	990
Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys	995	1000	1005
Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys	1010	1015	1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile	1025	1030	1035
Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys			

1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly 1055 1060 1065		
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala 1070 1075 1080		
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly 1085 1090 1095		
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu 1100 1105 1110		
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln 1115 1120 1125		
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu 1130 1135 1140		
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu 1145 1150 1155		
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu 1160 1165 1170		
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln 1175 1180 1185		
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp 1190 1195 1200		
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu 1205 1210 1215		
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val 1220 1225 1230		
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr 1235 1240 1245		
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys 1250 1255 1260		
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser 1265 1270 1275		
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala 1280 1285 1290		
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys 1295 1300 1305		
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala 1310 1315 1320		
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys 1325 1330 1335		

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
 1340 1345 1350
 Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
 1355 1360 1365
 Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
 1370 1375 1380
 Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
 1385 1390 1395
 Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
 1400 1405 1410
 Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
 1415 1420 1425
 Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
 1430 1435 1440
 Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
 1445 1450 1455
 Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
 1460 1465 1470
 Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
 1475 1480 1485
 Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
 1490 1495 1500
 Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
 1505 1510 1515
 Glu Cys Gly Cys Leu Ala Cys Ser
 1520

<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttgcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100
gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350
gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550
cctgtccgag tggaaaaaag gctgtgaggt ttctaaact ggaactggac 600
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650
cctgtgtcat cttgtcccggt ttctcccaa tattccttct caaacttggg 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750
gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
 1 5 10 15
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
 ctcatgggct gcctgggtcac aggc 24

<210> 206
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 206
 ccagtcggac aggtctctcc cctc 24

<210> 207
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 207
 tcagtgacca aggctgagca ggcg 24

<210> 208
 <211> 47
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 208
 ctacactcgt tgcaaactgg caaaaatatt ctcgagggtt ggcctgg 47

<210> 209
 <211> 1648
 <212> DNA
 <213> Homo sapiens

<400> 209
 caggccattt gcatcccaact gtccttgtgt tcggagccag gccacaccgt 50
 cctcagcagt gtcattgtgtt aaaaacgcca agctgaatat atcatgcccc 100
 tattaataact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
 ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
 gcggaagaag atcctatattt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
 gaggaatata ccacaggcat ggcagactgc atcttagtca acagccagtt 350
 cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
 ctgatgtcct ctatccatct ctaaagtgtca ccagctttga ctcagttggt 450
 cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500
 ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550
 ccctagtaca gctgctgga agattgacat cccaagattg ggagaggggt 600
 catctgatcg tggcaggtgg ttatgacgag agagtcctgg agaagtgtga 650
 acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700
 atgtgacctt cttgaggtct ttctcagaca aacagaaaaat ctccctctc 750
 cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800
 tgtccctctg gaagccatgt acatgcagtg ccagtcatt gctgttaatt 850
 cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900
 gagcctgacc cgggtgcactt ctgagaagca atagaaaagt tcatccgtga 950
 accttcctta aaagccacca tgggcctggc tggagagcc agagtgaagg 1000
 aaaaattttc ccctgaagca ttacagaac agctctaccg atatgttacc 1050
 aaactgctgg tataatcaga ttgtttttaa gatctccatt aatgtcattt 1100
 ttatggattg tagaccaggt ttgaaacca aaaaagaaac ctagaatcta 1150
 atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200
 ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250
 tttatgctat aatcattcca aattttgcca gtgttaagtt acaaatgtgg 1300
 tgtcattcca tgttcagcag agtattttta ttatattttc tcgggattat 1350
 tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400
 atagtttaag tgtgtatcat tatcaaagtt gattaatttg gttcatagt 1450
 ataatgagag cagggtatt gttagttcca gattcaatcc accgaagtgt 1500
 tcaactgcat ctgttaggga atttttgttt gtcctgtctt tgcctggatc 1550
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600
 actgagatat aataaaagggt gtttatcata aaaaaaaaaa aaaaaaaa 1648

<210> 210
 <211> 323

<212> PRT
 <213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	15
1				5					10						
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	30
				20					25						
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	45
				35					40						
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	60
				50					55						
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	75
				65					70						
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	90
				80					85						
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	105
				95					100						
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	120
				110					115						
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	135
				125					130						
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	150
				140					145						
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	165
				155					160						
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	180
				170					175						
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	195
				185					190						
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	210
				200					205						
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	225
				215					220						
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	240
				230					235						
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	255
				245					250						
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	270
				260					265						

Pro	Asp	Pro	Val	His	Phe	Ser	Glu	Ala	Ile	Glu	Lys	Phe	Ile	Arg
				275					280					285
Glu	Pro	Ser	Leu	Lys	Ala	Thr	Met	Gly	Leu	Ala	Gly	Arg	Ala	Arg
				290					295					300
Val	Lys	Glu	Lys	Phe	Ser	Pro	Glu	Ala	Phe	Thr	Glu	Gln	Leu	Tyr
				305					310					315
Arg	Tyr	Val	Thr	Lys	Leu	Leu	Val							
				320										

<210> 211
 <211> 1554
 <212> DNA
 <213> Homo sapiens

<400> 211
 gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50
 cttcgcgac ttcgccgtta ccttcttgct ggcgttggtg ggagccgtgc 100
 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200
 tttgcatgag ttcctgggta atttgcatga gagatatggg cctgtggtct 250
 ccttctggtt tggcaggcgc ctctgtggtta gtttgggcac tgttgatgta 300
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
 agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
 gttttgctat gaagtctggt acacagatgg taatgggtag tacatttgaa 600
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
 tggctacttca ggatcctaata acttggccat ctccacacaa gtttgatcca 1200
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
 ggacagggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400
 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgttaaa ttgattgagg aaaacaacca ttttaaaaaa atctatgttg 1500
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212
 <211> 462
 <212> PRT
 <213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu	1	5	10	15
Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala	20	25	30	
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu	35	40	45	
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn	50	55	60	
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg	65	70	75	
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His	80	85	90	
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys	95	100	105	
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn	110	115	120	
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu	125	130	135	
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu				

140										145					150				
Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln	His	Val	Pro	Leu	Ser					
				155					160					165					
Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val	Thr	Gln	Met	Val					
				170					175					180					
Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile	Arg	Phe	Gln					
				185					190					195					
Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly	Phe	Leu					
				200					205					210					
Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr	Glu					
				215					220					225					
Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys					
				230					235					240					
Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser					
				245					250					255					
Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser					
				260					265					270					
Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys					
				275					280					285					
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys					
				290					295					300					
Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val					
				305					310					315					
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu					
				320					325					330					
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln					
				335					340					345					
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg					
				350					355					360					
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro					
				365					370					375					
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp					
				380					385					390					
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly					
				395					400					405					
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr					
				410					415					420					
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val					
				425					430					435					

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
 455 460

<210> 213
 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 213
 ctagatttgt cggcttgccg ggagacttca ggagtcgctg tctctgaact 50
 tccagcctca gagaccgccg cccttgcccc cgagggccat gggccgggtc 100
 tcagggttg tgccctctcg ctccctgacg ctccctggcg atctggtggt 150
 cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250
 gccgcgtct ctgtcaccct gggcctcttt gcagtggagc tggccgggtt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
 gggctcactg tagtgcatcc gtggccctgt ccttcttcat attcgagcgt 400
 tgggagtgca ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450
 agctgtcact gaaatggctt tttcgtcac cgtctttggg ctgaaaaaga 500
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
 ttccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
 tgtttttag tagtaattaag acttatatac agtttttagg gacaattaa 750
 aaaaaaaaa 759

<210> 214
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 214
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
 1 5 10 15
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
 20 25 30
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
 35 40 45

Tyr	Asp	Lys	Gln	Asp	Ile	Gln	Leu	Val	Ala	Ala	Leu	Ser	Val	Thr	50	55	60
Leu	Gly	Leu	Phe	Ala	Val	Glu	Leu	Ala	Gly	Phe	Leu	Ser	Gly	Val	65	70	75
Ser	Met	Phe	Asn	Ser	Thr	Gln	Ser	Leu	Ile	Ser	Ile	Gly	Ala	His	80	85	90
Cys	Ser	Ala	Ser	Val	Ala	Leu	Ser	Phe	Phe	Ile	Phe	Glu	Arg	Trp	95	100	105
Glu	Cys	Thr	Thr	Tyr	Trp	Tyr	Ile	Phe	Val	Phe	Cys	Ser	Ala	Leu	110	115	120
Pro	Ala	Val	Thr	Glu	Met	Ala	Leu	Phe	Val	Thr	Val	Phe	Gly	Leu	125	130	135
Lys	Lys	Lys	Pro	Phe											140		

<210> 215
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 215
 tcccggaacc tgccgccttg ccactatgtc ccgcccgtct atgctgcttg 50
 cctgggctct cccagcctc ctgcgactcg gagcggtca ggagacagaa 100
 gaccggcct gctgcagccc catagtgcc cggaacgagt ggaaggcct 150
 ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
 tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
 cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
 tccattggca tcagcttcac gggcaactac atggatcggg tgccacacc 450
 ccaggccatc cgggcagccc agggctctact ggctgcggg gtggctcagg 500
 gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
 acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
 ctaccgtcc cctgagggcc ctgctgatcc gcacccatt cctccctcc 650
 catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216
 <211> 196
 <212> PRT

<213> Homo sapiens

<400> 216

```
Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu
 1           5           10           15
Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
           20           25           30
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
           35           40           45
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
           50           55           60
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
           65           70           75
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
           80           85           90
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
           95          100          105
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
          110          115          120
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
          125          130          135
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
          140          145          150
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
          155          160          165
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
          170          175          180
Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
          185          190          195
```

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

```
ctgggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag 50
gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100
tctatctggt catctgtggc caggatgatg gtccctcccg ctcagaggac 150
cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcggaa 200
```

gcggggccac atctcaccta agtcccgcc catggccaat tccactctcc 250
 tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300
 cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350
 ctttggttg ggcgacttct actccaacat caagacggtg gccctgaacc 400
 tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
 cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500
 gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550
 aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
 gaacggggcc gccggacctc gctttgcacc cacgaccag ccaagatctg 650
 ctcccagac cacgctcaga gctcagccac ctggagctgc tcccagccct 700
 tcaaagtcgt ctgtgtctac atcgcttct acagcacgga ctatcggtg 750
 gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800
 cccatctggg tgaccgggg caggccacag aggccaggcc agggctggaa 850
 ggacaggcct gcccatgcag gagaccatct ggacaccggg caggaagg 900
 gttgggcctc aggcaggag gggggtggag acgaggagat gccaagtggg 950
 gccagggcc agtctcaagt ggcagagaaa ggggcccaag tgctggtccc 1000
 aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagt 1050
 ggctctctgt gcagcctcac agggctttgc cacggagcca cagagagatg 1100
 ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150
 gtcagggag gaagctaagc ccttggttct tgccatcctg aggaaagata 1200
 gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250
 atggatggct gagagggtt cctaggagcc agtcagcagg gtgggggtgg 1300
 gccagaggag ctctccagcc ctgcctagt ggcgcctga gcccttgtc 1350
 gtgtgtcag catggcatga ggctgaagt gcaaccctgg ggtctttgat 1400
 gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaa 1450
 ttccctctc tgccagtact cccctgtac caccattgc tgatggcaca 1500
 cccatcctta agctaagaca ggacgattgt ggtcctcca cactaaggcc 1550
 acagcccatc cgcgtgctgt gtgtccctct tccacccaa cccctgctgg 1600
 ctctctggg agcatccatg tccggagag ggtccctca acagtcagcc 1650

tcacctgtca gaccgggggtt ctcccggatc tggatggcgc cgccctctca 1700
gcagcgggca cgggtggggc ggggccgggc cgcagagcat gtgctggatc 1750
tggtctgtgt gtctgtctgt ggggtggggg aggggaggga agtcttgtga 1800
aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850
aataaagctt gccccggggc a 1871

<210> 218
<211> 252
<212> PRT
<213> Homo sapiens

<400> 218
Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser
1 5 10 15
Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser
20 25 30
Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
35 40 45
Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met
50 55 60
Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
65 70 75
Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
80 85 90
Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
95 100 105
Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
110 115 120
Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
125 130 135
His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro
140 145 150
Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile
155 160 165
Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu
170 175 180
Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro
185 190 195
Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
 215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
 230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
 245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

gtgaatgtga gggtttgatg actttcagat gtctaggaac cagagtgggt 50
 gcagggggccc caggcagggc tgattcttgg gcggaggaga gtagggtaaa 100
 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150
 agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200
 gcgcccgcgc cgccgtcgct cctgcagcgc tgctcgaccta gccgctagca 250
 tcttcccagag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300
 agcgccagcc ggctgcggtc gccacacgg ctcaccatgg gctccgggcg 350
 ccggggcgctg tccgcggtgc cggccgtgct gctggctctc acgctgccgg 400
 ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450
 aagtgtctgg tgggtgtgca ctcgaacccg gccacggact ccaagggctc 500
 ctcttctctcc ccgctgggga tatcggtccg ggcggccaac tccaaggctc 550
 ccttctcggc ggtgcgagc accaaccag agccatccga gatgagcaac 600
 aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650
 tttcacattg gagtctgtct ttgtagcacc aagaaaagg atttacagtt 700
 tcagttttca cgtgattaaa gtctaccaga gccaaaactat ccaggttaac 750
 ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800
 tgttactcgt gaagctgcc cgaatggtgt cctgctctac ctagataaag 850
 aggataaggt ttacctaaaa ctggagaaag gtaatttggg tggaggctgg 900
 cagtattcca cgttttctgg ctttctgggtg ttccccctat aggattcaat 950
 ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000
 gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050
 ggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100

tcacagatta tttgtgtgtg tctgtttcag tatatttga ttgggactct 1150
 aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200
 acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250
 gaattttatt tgtttagttt taaaagactg gcaaccaggt ctaaggatta 1300
 gaaaactcta aagttctgac ttcaatcaac ggtagtgtg atactgcaa 1350
 agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400
 ggaattagtt tgtttggttc ttgtaaaaaa cttggatttt ttttttcagt 1450
 aactgggtatt atgttttctc ttaaaataag gtaatgaatg gcttgcccac 1500
 aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaa 1550
 gaatgcttca tagttgtatt ttaattgtat atgtgaaaga gtcataattt 1600
 ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650
 aaagttgctt acccaaaatc taagtgtc atccctgagc ctcagcaaaa 1700
 cagctccct ccgagggaaa tcttatactt tattgtcaa ctttaattaa 1750
 aatgattgat aataaccact ttattaa cctaaggttt ttttttttct 1800
 cgtagacatg accactttat taactggtgg tgggatgctg ttgtttctaa 1850
 ttatacctat ttttcaaggc ttctgttgta tttgaagtat catctgggtt 1900
 tgcttaact ctttaaattg tatatattta tctgtttagc taatattaa 1950
 ttcaaataat ccataatctaa atttagtgca atatcttgtc tttgtatag 2000
 gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050
 tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met	Gly	Ser	Gly	Arg	Arg	Ala	Leu	Ser	Ala	Val	Pro	Ala	Val	Leu
1				5				10						15

Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp
			20						25					30

Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
			35					40						45

Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
			50					55						60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
					65				70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
					80				85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
					95				100					105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
					110				115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
					125				130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
					140				145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
					155				160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
					170				175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
					185				190					195	
Phe	Leu	Val	Phe	Pro	Leu										
					200										

<210> 221
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 221
 acggctcacc atgggctccg 20

<210> 222
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 222
 aggaagagga gcccttgag tccg 24

<210> 223
 <211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
cgtgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
cggtagccat gactgcggcc gtgttcttcg gctgcgcctt cattgccttc 50
gggcctgcgc tcgcccttta tgtcttcacc atcgccatcg agccgttgcg 100
tatcatcttc ctcacgcgcg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300
gtgaaggttt gaagagtata aaccaggtg agacagcacc ctctatgcga 350
ctgctggcct atgtttcttg cttgggcttt ggaatcatga gtggagtatt 400
ttcctttgtg aataccctat ctgactcctt ggggccaggc acagtgggca 450
ttcatggaga ttctctcaa ttcttccttt attcagcttt catgacgctg 500
gtcattatct tgctgcatgt attctggggc attgtatttt ttgatggctg 550
tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc 600
tgggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650
tcagcattta taatcctggt gctcatgggc acctgggcat tcttagctgc 700
gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750
actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800
tcccaaaccg cagactacat ctttagagga agcacaactg tgcctttttc 850
tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900
ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly	
1				5					10					15	
Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu	
				20					25					30	
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	
				35					40					45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	
				50					55					60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	
				65					70					75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	
				80					85					90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	
				95					100					105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
				110					115					120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
				125					130					135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
				140					145					150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
				155					160					165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
				170					175					180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
				185					190					195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
				200					205					210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
				215					220					225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
				230					235					240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	
				245					250					255	

Ser Arg

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226
cggcaaccag ccgccgccac caccgctgcc actgccgccc tgccggggcc 50
atgttcgctc tgggcttgcc cttcttggtg ctcttggtgg cctcggtcga 100
gagccatctg ggggttcttg ggccaagaa cgtctcgag aaagacgccg 150
agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200
tacaccttca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250
gtctgtgaac gtctgaaca agcagaagg ggcgccgttg ctgtttgttg 300
tccgccagaa ggaggctgtg gtgtccttcc aggtgcccct aatcctgcga 350
gggatgtttc agcgcaagta cctctaccaa aaagtggaac gaaccctgtg 400
tcagcccccc accaagaatg agtcggagat tcagttcttc tacgtggatg 450
tgtccacct gtcaccagtc aacaccacat accagctccg ggtcagccgc 500
atggacgatt ttgtgctcag gactggggag cagttcagct tcaataccac 550
agcagcacag cccagctact tcaagtatga gttccctgaa ggcgtggact 600
cggtaattgt caaggtgacc tccaacaagg cttccccctg ctcagtcac 650
tccattcagg atgtgctgtg tcctgtctat gacctggaca acaacgtagc 700
cttcacggtc atgtaccaga cgatgaccaa gaaggcggcc atcacgtac 750
agcgcaaaga cttccccagc aacagctttt atgtggtggt ggtggtgaag 800
accgaagacc aagcctgcgg gggctccctg ctttctacc ctttcgcaga 850
agatgaaccg gtcgatcaag ggcaccgcca gaaaaccctg tcagtgtctg 900
tgtctcaagc agtcacgtct gaggcatacg tcagtgggat gctcttttgc 950
ctgggtatat ttctctcctt ttacctgctg accgtcctcc tggcctgctg 1000
ggagaactgg aggcagaaga agaagacct gctggtggcc attgaccgag 1050
cctgccaga aagcggtcac cctcgagtcc tggctgattc tttcctggc 1100
agttccccct atgagggtta caactatggc tcctttgaga atgtttcttg 1150
atctaccgat ggtctggttg acagcgctgg cactggggac ctctcttacg 1200
gttaccaggg ccgctccttt gaacctgtag gtactcggcc ccgagtggac 1250
tccatgagct ctgtggagga ggatgactac gacacattga ccgacatcga 1300
ttccgacaag aatgtcattc gcaccaagca atacctctat gtggctgacc 1350

tggcacggaa ggacaagcgt gttctgcgga aaaagtacca gatctacttc 1400
 tggaaacattg ccaccattgc tgtctttctat gcccttcctg tggcgcagct 1450
 ggtgatcacc taccagacgg tggatgaatgt cacagggaat caggacatct 1500
 gctactacaa ctctctctgc gccacccac tgggcaatct cagcgccttc 1550
 aacaacatcc tcagcaacct ggggtacatc ctgctggggc tgcttttcct 1600
 gctcatcatc ctgcaacggg agatcaacca caaccgggccc ctgctgcgca 1650
 atgacctctg tgccctggaa tgtgggatcc ccaaactt tgggcttttc 1700
 tacgccatgg gcacagccct gatgatggag gggctgctca gtgcttgcta 1750
 tcatgtgtgc cccaactata ccaatttcca gtttgacaca tcgttcatgt 1800
 acatgatcgc cggactctgc atgctgaagc tctaccagaa ggggcacccg 1850
 gacatcaacg ccagcgccta cagtgcctac gcctgcctgg ccattgtcat 1900
 ctctctctct gtgctgggag tggcttttgg caaagggaac acggcgcttc 1950
 ggatcgtctt ctccatcatt cacatcatcg ccacctgct cctcagcacg 2000
 cagctctatt acatgggccc gtggaaactg gactcgggga tcttcgcgcg 2050
 catcctccac gtgctctaca cagactgcat ccggcagtc agcgggcccgc 2100
 tctacgtgga ccgcatggtg ctgctgggca tgggcaacgt catcaactgg 2150
 tcgtggctg cctatgggct tatcatgcgc ccaatgatt tcgcttcta 2200
 cttgttgccc attggcatct gcaacctgct cctttacttc gccttctaca 2250
 tcatcatgaa gctccggagt ggggagagga tcaagctcat cccctgctc 2300
 tgcacggttt gcacctccgt ggtctggggc ttgcgctct tcttcttctt 2350
 ccagggactc agcacctggc agaaaacccc tgcagagtcg agggagcaca 2400
 accgggactg catcctctc gacttctttg acgaccacga catctggcac 2450
 ttcctctcct ccacgccc atctcgggtcc ttctgggtgt tgctgacact 2500
 ggatgacgac ctggatactg tgcagcggga caagatctat gtcttctagc 2550
 aggagctggg cccttcgctt cacctcaagg ggccctgagc tcctttgtgt 2600
 catagaccgg tcaactctgc gtgctgtggg gatgagtcac agcaccgctg 2650
 cccagcactg gatggcagca ggacagccag gtctagctta ggcttgccct 2700
 gggacagcca tggggtggca tggaaccttg cagctgccct ctgccgagga 2750
 gcaggcctgc tcccctggaa ccccagatg ttggccaaat tgctgctttc 2800

ttctcagtgt tggggccttc catgggcccc tgtcctttgg ctctccattt 2850
 gtccctttgc aagaggaagg atggaaggga caccctcccc atttcatgcc 2900
 ttgcattttg cccgtcctcc tccccacaat gccccagcct gggacctaag 2950
 gcctcttttt cctcccatac tcccactcca gggcctagtc tggggcctga 3000
 atctctgtcc tgtatcaggg ccccagttct ctttgggctg tccctggctg 3050
 ccatcactgc ccattccagt cagccaggat ggatgggggt atgagatttt 3100
 gggggttggc cagctgggtgc cagacttttg gtgctaaggc ctgcaagggg 3150
 cctggggcag tgcgtattct cttccctctg acctgtgctc agggctggct 3200
 ctttagcaat gcgctcagcc caatttgaga accgccttct gattcaagag 3250
 gctgaattca gaggtcacct cttcatccca tcagctccca gactgatgcc 3300
 agcaccagga ctggaggagg aagcgctca ccccttcctt tccttctttc 3350
 caggccctta gtcttgccaa accccagctg gtggcctttc agtgccattg 3400
 aactgcccc agaatgtcca ggggcaaagg agggatgata cagagttcag 3450
 cccgttctgc ctccacagct gtgggcaccc cagtgcctac cttagaaagg 3500
 ggcttcagga agggatgtgc tgtttccctc tacgtgcccc gtcctagcct 3550
 cgctctagga cccagggtctg gcttctaagt ttccgtccag tcttcaggca 3600
 agttctgtgt tagtcatgca cacacatacc tatgaaacct tggagtttac 3650
 aaagaattgc cccagctctg ggcaccctgg ccaccctggt ccttggatcc 3700
 ccttcgtccc acctggtcca cccagatgc tgaggatggg ggagctcagg 3750
 cggggcctct gctttgggga tgggaatgtg tttttctccc aaacttgttt 3800
 ttatagctct gcttgaaggg ctgggagatg aggtgggtct ggatcttttc 3850
 tcagagcgtc tccatgctat ggttgcattt ccgttttcta tgaatgaatt 3900
 tgcatccaat aaacaaccag actcaaaaaa aaaaaaaaaa 3939

<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met	Phe	Ala	Leu	Gly	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val	Ala	Ser
1				5					10					15

Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25					30

Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser		35	40	45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn		50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln		65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val		80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg		95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro		110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser		125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg		140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn		155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu		170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe		185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr		200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met		215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser		230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala		245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro		260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser		275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys		290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala		305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala				

320										325					330				
Ile	Asp	Arg	Ala	Cys	Pro	Glu	Ser	Gly	His	Pro	Arg	Val	Leu	Ala					
				335					340					345					
Asp	Ser	Phe	Pro	Gly	Ser	Ser	Pro	Tyr	Glu	Gly	Tyr	Asn	Tyr	Gly					
				350					355					360					
Ser	Phe	Glu	Asn	Val	Ser	Gly	Ser	Thr	Asp	Gly	Leu	Val	Asp	Ser					
				365					370					375					
Ala	Gly	Thr	Gly	Asp	Leu	Ser	Tyr	Gly	Tyr	Gln	Gly	Arg	Ser	Phe					
				380					385					390					
Glu	Pro	Val	Gly	Thr	Arg	Pro	Arg	Val	Asp	Ser	Met	Ser	Ser	Val					
				395					400					405					
Glu	Glu	Asp	Asp	Tyr	Asp	Thr	Leu	Thr	Asp	Ile	Asp	Ser	Asp	Lys					
				410					415					420					
Asn	Val	Ile	Arg	Thr	Lys	Gln	Tyr	Leu	Tyr	Val	Ala	Asp	Leu	Ala					
				425					430					435					
Arg	Lys	Asp	Lys	Arg	Val	Leu	Arg	Lys	Lys	Tyr	Gln	Ile	Tyr	Phe					
				440					445					450					
Trp	Asn	Ile	Ala	Thr	Ile	Ala	Val	Phe	Tyr	Ala	Leu	Pro	Val	Val					
				455					460					465					
Gln	Leu	Val	Ile	Thr	Tyr	Gln	Thr	Val	Val	Asn	Val	Thr	Gly	Asn					
				470					475					480					
Gln	Asp	Ile	Cys	Tyr	Tyr	Asn	Phe	Leu	Cys	Ala	His	Pro	Leu	Gly					
				485					490					495					
Asn	Leu	Ser	Ala	Phe	Asn	Asn	Ile	Leu	Ser	Asn	Leu	Gly	Tyr	Ile					
				500					505					510					
Leu	Leu	Gly	Leu	Leu	Phe	Leu	Leu	Ile	Ile	Leu	Gln	Arg	Glu	Ile					
				515					520					525					
Asn	His	Asn	Arg	Ala	Leu	Leu	Arg	Asn	Asp	Leu	Cys	Ala	Leu	Glu					
				530					535					540					
Cys	Gly	Ile	Pro	Lys	His	Phe	Gly	Leu	Phe	Tyr	Ala	Met	Gly	Thr					
				545					550					555					
Ala	Leu	Met	Met	Glu	Gly	Leu	Leu	Ser	Ala	Cys	Tyr	His	Val	Cys					
				560					565					570					
Pro	Asn	Tyr	Thr	Asn	Phe	Gln	Phe	Asp	Thr	Ser	Phe	Met	Tyr	Met					
				575					580					585					
Ile	Ala	Gly	Leu	Cys	Met	Leu	Lys	Leu	Tyr	Gln	Lys	Arg	His	Pro					
				590					595					600					
Asp	Ile	Asn	Ala	Ser	Ala	Tyr	Ser	Ala	Tyr	Ala	Cys	Leu	Ala	Ile					
				605					610					615					

Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	
				620					625					630	
Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	
				635					640					645	
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	
				650					655					660	
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	
				665					670					675	
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	
				680					685					690	
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	
				695					700					705	
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	
				710					715					720	
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	
				725					730					735	
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	
				740					745					750	
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	
				755					760					765	
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	
				770					775					780	
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	
				785					790					795	
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	
				800					805					810	
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln	
				815					820					825	
Arg	Asp	Lys	Ile	Tyr	Val	Phe									
				830											

<210> 228
 <211> 2848
 <212> DNA
 <213> Homo sapiens

<400> 228
 gctcaagtgc cctgccttgc cccacccagc ccagcctggc cagagccccc 50
 tggagaagga gctctcttct tgcttggcag ctggaccaag ggagccagtc 100
 ttgggcgctg gagggcctgt cctgaccatg gtccctgcct ggctgtggct 150
 gctttgtgtc tccgtccccc aggctctccc caaggcccag cctgcagagc 200

tgtctgtgga agttccagaa aactatggtg gaaatttccc tttataacctg 250
 accaagttgc cgctgccccg tgagggggct gaaggccaga tcgtgctgtc 300
 aggggactca ggcaaggcaa ctgagggccc atttgctatg gatccagatt 350
 ctggcttcct gctggtgacc agggccctgg accgagagga gcaggcagag 400
 taccagctac aggtcaccct ggagatgcag gatggacatg tcttgtgggg 450
 tccacagcct gtgcttgtgc acgtgaagga tgagaatgac caggtgcccc 500
 atttctctca agccatctac agagctcggc tgagccgggg taccaggcct 550
 ggcatccctt tcctcttcct tgaggcttca gaccgggatg agccaggcac 600
 agccaactcg gatcttcgat tccacatcct gagccaggct ccagcccagc 650
 cttccccaga catgttccag ctggagcctc ggctgggggc tctggccctc 700
 agccccaagg ggagcaccag ccttgaccac gccctggaga ggacctacca 750
 gctgttggta caggtcaagg acatgggtga ccaggcctca ggccaccagg 800
 ccactgccac cgtggaagtc tccatcatag agagcacctg ggtgtcccta 850
 gagcctatcc aactggcaga gaatctcaaa gtcctatacc cgcaccacat 900
 ggcccaggta cactggagtg ggggtgatgt gcactatcac ctggagagcc 950
 atcccccggg accctttgaa gtgaatgcag agggaaacct ctacgtgacc 1000
 agagagctgg acagagaagc ccaggctgag tacctgctcc aggtgcgggc 1050
 tcagaattcc catggcgagg actatgcggc ccctctggag ctgcacgtgc 1100
 tggatgatga tgagaatgac aacgtgccta tctgccctcc ccgtgacccc 1150
 acagtacgca tccctgagct cagtccacca ggtactgaag tgactagact 1200
 gtcagcagag gatgcagatg cccccggctc cccaattcc cacgttgtgt 1250
 atcagctcct gagccctgag cctgaggatg gggtagaggg gagagccttc 1300
 caggtggacc ccaattcagg cagtgtgacg ctgggggtgc tccactccg 1350
 agcaggccag aacatcctgc ttctggtgct ggccatggac ctggcaggcg 1400
 cagaggggtg cttcagcagc acgtgtgaag tcgaagtcgc agtcacagat 1450
 atcaatgatc acgcccctga gttcatcact tcccagattg ggcctataag 1500
 cctccctgag gatgtggagc ccgggactct ggtggccatg ctaacagcca 1550
 ttgatgctga cctcagagccc gccttcggcc tcatggattt tgccattgag 1600
 aggggagaca cagaaggagc ttttggcctg gattgggagc cagactctgg 1650

gcatgttaga ctcagactct gcaagaacct cagttatgag gcagctccaa 1700
 gtcattgaggt ggtggtggtg gtgcagagtg tggcgaagct ggtggggcca 1750
 ggcccaggcc ctggagccac cgccacggtg actgtgctag tggagagagt 1800
 gatgccaccc cccaagttgg accaggagag ctacgaggcc agtgtcccca 1850
 tcagtgcacc agccggctct ttcctgctga ccatccagcc ctccgacccc 1900
 atcagccgaa ccctcaggtt ctccctagtc aatgactcag agggctggct 1950
 ctgcattgag aaattctccg gggaggtgca caccgcccag tccctgcagg 2000
 gcgcccagcc tggggacacc tacacggtgc ttgtggaggc ccaggataca 2050
 gccctgactc ttgccctgt gccctcccaa tacctctgca caccgcccga 2100
 agaccatggc ttgatcgtga gtggaccag caaggacccc gatctggcca 2150
 gtgggcacgg tccctacagc ttcacccttg gtcccaaccc cacggtgcaa 2200
 cgggattggc gcctccagac tctcaatggt tcccatgcct acctcacctt 2250
 ggccctgcat tgggtggagc cagtggaaca cataatcccc gtggtggtca 2300
 gccacaatgc ccagatgtgg cagctcctgg ttcgagtgat cgtgtgtcgc 2350
 tgcaacgtgg aggggcagtg catgcgcaag gtgggccgca tgaaggcat 2400
 gccacgaag ctgtcggcag tgggcacctt tgtaggcacc ctggtagcaa 2450
 taggaatctt cctcatctc attttcaccc actggaccat gtcaaggaag 2500
 aaggacccgg atcaaccagc agacagcgtg cccctgaagg cgactgtctg 2550
 aatggcccag gcagctctag ctgggagctt ggcctctggc tccatctgag 2600
 tcccctggga gagagcccag caccgaagat ccagcagggg acaggacaga 2650
 gtagaagccc ctccatctgc cctgggggtg aggcaccatc accatcacca 2700
 ggcatgtctg cagagcctgg acaccaactt tatggactgc ccatgggagt 2750
 gctccaaatg tcagggtgtt tgcccaataa taaagcccca gagaactggg 2800
 ctgggcccta tgggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaag 2848

<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
1					5				10				15	

Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

20										25					30				
Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro					
				35					40					45					
Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp					
				50					55					60					
Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser					
				65					70					75					
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala					
				80					85					90					
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val					
				95					100					105					
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn					
				110					115					120					
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
				125					130					135					
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
				140					145					150					
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
				155					160					165					
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
				170					175					180					
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
				185					190					195					
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
				200					205					210					
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
				215					220					225					
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
				230					235					240					
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
				245					250					255					
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
				260					265					270					
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
				275					280					285					
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
				290					295					300					
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
				305					310					315					

Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn	
				320					325					330	
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile	
				335					340					345	
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	
				350					355					360	
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	
				365					370					375	
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	
				380					385					390	
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	
				395					400					405	
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met	
				410					415					420	
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	
				425					430					435	
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	
				440					445					450	
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	
				455					460					465	
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	
				470					475					480	
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	
				485					490					495	
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	
				500					505					510	
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	
				515					520					525	
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	
				530					535					540	
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	
				545					550					555	
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	
				560					565					570	
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	
				575					580					585	
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	
				590					595					600	
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly	

605	610	615
Glu Val His Thr Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly Asp	
620	625	630
Thr Tyr Thr Val Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr Leu	
635	640	645
Ala Pro Val Pro Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp His	
650	655	660
Gly Leu Ile Val Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala Ser	
665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr Val	
680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu	Asn Gly Ser His Ala Tyr	
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu	Pro Arg Glu His Ile Ile	
710	715	720
Pro Val Val Val Ser His Asn Ala Gln	Met Trp Gln Leu Leu Val	
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val	Glu Gly Gln Cys Met Arg	
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro	Thr Lys Leu Ser Ala Val	
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu Ile	
770	775	780
Leu Ile Phe Thr His Trp Thr Met Ser	Arg Lys Lys Asp Pro Asp	
785	790	795
Gln Pro Ala Asp Ser Val Pro Leu Lys	Ala Thr Val	
800	805	

<210> 230
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 230
 cgccttaccg cgcagcccga agattcacta tgggtgaaaat cgccttcaat 50

<210> 231
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
<221> Artificial Sequence
<222> full
<223> Synthetic oligonucleotide probe

<400> 231
cctgagctgt aaccccactc cagg 24

<210> 232
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
agagtctgtc ccagctatct tgt 23

<210> 233
<211> 2786
<212> DNA
<213> Homo sapiens

<400> 233
ccggggacat gaggtggata ctgttcattg gggcccttat tgggtccagc 50
atctgtggcc aagaaaaatt ttttggggac caagttttga ggattaatgt 100
cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200
gatgtcctgg tcccatctgt cagtctgcag gcatttaaata ccttcctgag 250
atcccagggc ttagagtacg cagtgcacaat tgaggacctg caggcccttt 300
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400
cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
actgggaaag gcgtgaggcg gccggccggt tggctgaatg caggcatcca 550
ttcccagagag tggatctccc aggccactgc aatctggacg gcaaggaaga 600
ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650
atggatattt tcttggtgcc tgtggccaat cctgatggat atgtgtatac 700
tcaaactcaa aaccgattat ggaggaagac gcgggtccga aatcctggaa 750
gctcctgcat tgggtgctgac ccaaatagaa actggaacgc tagttttgca 800
ggaaagggag ccagcgacaa cccttgctcc gaagtgtacc atggaccca 850

cgccaattcg gaagtggagg tgaaatcagt ggtagatttc atccaaaaac 900
 atgggaatth caagggcttc atcgacctgc acagctactc gcagctgctg 950
 atgtatccat atgggtactc agtcaaaaag gccccagatg ccgaggaact 1000
 cgacaagggtg gcgaggcttg cggccaaagc tctggcttct gtgtcgggca 1050
 ctgagtacca agtgggtccc acctgcacca ctgtctatcc agctagcggg 1100
 agcagcatcg actgggcgta tgacaacggc atcaaatttg cattcacatt 1150
 tgagttgaga gataccggga cctatggctt cctcctgcca gctaaccaga 1200
 tcatccccac tgcagaggag acgtggctgg ggctgaagac catcatggag 1250
 catgtgcggg acaacctcta ctaggcgatg gctctgctct gtctacattt 1300
 atttgtaccc acacgtgcac gcactgaggc cattgttaaa ggagctcttt 1350
 cctacctgtg tgagtcagag ccctctgggt ttgtggagca cacaggcctg 1400
 cccctctcca gccagctccc tggagtcgtg tgtcctggcg gtgtccctgc 1450
 aagaactggt tctgccagcc tgctcaattt tggctcctgt gtttttgatg 1500
 agccttttgt ctgtttctcc ttccaccctg ctggctgggc ggctgcactc 1550
 agcatcacc cttcctgggt ggcatgtctc tctctacctc atttttagaa 1600
 ccaaagaaca tctgagatga ttctctaccc tcatccacat ctagccaagc 1650
 cagtgcactt gctctgggtg cactgtggga gacaccactt gtcttttaggt 1700
 gggctcmeta gatgatgtag aatttccttt aatttctcgc agtcttctg 1750
 gaaaatattt tcctttgagc agcaaactct gtaggatat cagtgaagg 1800
 ctctccctcc ctctctctct gttttttttt tttttgagac agagttttgc 1850
 tcttgttgcc caggctggag tgtgatggct cgatcttggc tcaccacaac 1900
 ctctgcctcc tgggttcaag caattctct gcctcagcct cttgagtagc 1950
 ttggtttata ggcgcctgcc accatgcctg gctaattttg tgtttttagt 2000
 agagacaggg tttctccatg ttggctcaggc tggctcmeta ctcccaacct 2050
 caggatgatc gccctccttg gcctcccaga gtgctgggat tacagggtgtg 2100
 agccactgtg ccgggcccgt cccctccttt tttaggcctg aatacaaagt 2150
 agaagatcac tttccttcac tgtgtcgaga atttctagat actacagttc 2200
 ttactcctct cttccctttg ttattcagtg tgaccaggat ggccggaggg 2250
 gatctgtgtc actgtaggta ctgtgccag gaaggctggg tgaagtgacc 2300

atctaaattg caggatgggtg aaattatccc catctgtcct aatgggctta 2350
 cctcctcttt gccttttgaa ctcaacttcaa agatctaggc ctcatcttac 2400
 aggtcctaaa tcactcatct ggcctggata atctcactgc cctggcacat 2450
 tcccatttgt gctgtgggtg atcctgtgtt tccttgtcct ggtttgtgtg 2500
 tgtgtgtgtg tgtgtgtgtg tgtgtgtgtt tgtgtgtgtg tgtctgtcta 2550
 ttttgatatcc tggaccacaa gttcctaagt agagcaagaa ttcacaaacc 2600
 agctgcctct tgtttcattt cacctcagca cgtaccatct gtccttttgt 2650
 tgttgttgtt ttgttttgtt ttttttgctt ttaccaaaca tgtctgtaaa 2700
 tcttaacctc ctgcctagga tttgtacagc atctgggtgtg tgcttataag 2750
 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile
1				5					10					15
Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165

Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	185	190	195
Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	200	205	210
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	215	220	225
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	230	235	240
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	245	250	255
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	260	265	270
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	275	280	285
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	290	295	300
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	305	310	315
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	320	325	330
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	335	340	345
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	350	355	360
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	365	370	375
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	380	385	390
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	395	400	405
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	410	415	420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 235

caaccatgca aggacagggc aggagaagag gaacctgcaa agacatattt 50
tggtccaaaa tggcatctta cctttatgga gtactctttg ctgttggcct 100
ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150
cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200
aacaccgact ttgccttccg cctataccgc aggtctggtt tggagacccc 250
gagtcagaac atcttcttct cccctgtgag tgtctccact tccctggcca 300
tgctctccct tggggcccac tcagtcacca agaccagat tctccagggc 350
ctgggcttca acctcacaca cacaccagag tctgccatcc accagggctt 400
ccagcacctg gttcactcac tgactgttcc cagcaaagac ctgaccttga 450
agatgggaag tgccctcttc gtcaagaagg agctgcagct gcaggcaaatt 500
ttcttgggca atgtcaagag gctgtatgaa gcagaagtct tttctacaga 550
tttctccaac cctccattg cccaggcgag gatcaacagc catgtgaaaa 600
agaagacca aggaaggtt gtagacataa tccaaggcct tgaccttctg 650
acggccatgg ttctggtgaa tcacattttc tttaaagcca agtgggagaa 700
gccctttcac cttgaatata caagaaagaa cttcccatc ctggtgggcg 750
agcaggtcac tgtgcaagtc cccatgatgc accagaaaga gcagttcgct 800
tttggggtgg atacagagct gaactgcttt gtgctgcaga tggattacaa 850
gggagatgcc gtggccttct ttgtcctccc tagcaagggc aagatgaggc 900
aactggaaca ggccttgtca gccagaacac tgataaagtg gagccactca 950
ctccagaaaa ggtggataga ggtgttcac cccagatttt ccatttctgc 1000
ctctacaat ctggaaacca tctcccgaa gatgggcac caaatgcct 1050
ttgacaaaaa tgctgatttt tctggaattg caaagagaga ctccctgcag 1100
gtttctaaag caaccacaa ggctgtgctg gatgtcagt aagagggcac 1150
tgagggcaca gcagctacca ccaccaagtt catagtccga tcgaaggatg 1200
gtccctctta cttcactgtc tccttcaata ggaccttct gatgatgatt 1250
acaaataaag ccacagacgg tattctcttt ctagggaag tggaaaatcc 1300
cactaaatcc taggtgggaa atggcctgtt aactgatggc acattgctaa 1350
tgcacaagaa ataacaaacc acatccctct ttctgttctg aggggtgcatt 1400
tgaccccgat ggagctggat tcgctggcag ggatgccact tccaaggctc 1450

aatcaccaaa ccatcaacag ggacccagc cacaagccaa caccattaa 1500
 cccagtcag tgcccttttc cacaaattct cccaggtaac tagcttcatg 1550
 ggatgttgct gggttacat atttccattc cttggggctc ccaggaatgg 1600
 aaatacgcca acccaggtta ggcacctcta ttgcagaatt acaataaac 1650
 attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236
 Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys
 1 5 10 15
 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
 20 25 30
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
 35 40 45
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
 50 55 60
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
 65 70 75
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
 80 85 90
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
 95 100 105
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
 110 115 120
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
 125 130 135
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
 140 145 150
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
 155 160 165
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
 170 175 180
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
 185 190 195
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

200	205	210
Lys Trp Glu Lys Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn Phe	
215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr	Val Gln Val Pro Met Met	
230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu Asn	
245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala Phe	
260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln Ala	
275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp	Ser His Ser Leu Gln Lys	
290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala Ser	
305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn Ala	
320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp Ser	
335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys	Ala Val Leu Asp Val Ser	
350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe Ile	
365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe Asn	
380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn	Lys Ala Thr Asp Gly Ile	
395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro	Thr Lys Ser	
410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgggg tctccaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggtataggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactctttgc tgttgacctc tgtgctcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
ggctgaccgt gctacattgc ctggaggaag cctaaggaaac ccaggcatcc 50

agctgcccac gcctgagtcc aagattcttc ccaggaacac aaacgtagga 100
 gacccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150
 ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200
 ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250
 aaaggaaatg ttctccttat gtttgggtcta ctattgcatt tagaagctgc 300
 aacaaattcc aatgagacta gcacctctgc caaacttga tccagtgtga 350
 tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400
 agtgggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450
 ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500
 gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata 550
 gccaccaact ctgagtccag cacaacctcc agtggggcca gcacagccac 600
 caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact 650
 ctgggtccag tgtgacctcc agtggagcca gcaactgccac caactctgag 700
 tccagcacag tgtccagtag ggccagcact gccaccaact ctgagtctag 750
 cacactctcc agtggggcca gcacagccac caactctgac tccagcaca 800
 cctccagtgg ggctagcaca gccaccaact ctgagtccag cacaacctcc 850
 agtggggcca gcacagccac caactctgag tccagcacag tgtccagtag 900
 ggccagcact gccaccaact ctgagtccag cacaacctcc agtggggcca 950
 gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca 1000
 gccaccaact ctgagtccag cagacctcc agtggggcca gcacagccac 1050
 caactctgac tccagcacag tgtccagtgg ggccagcact gccaccaact 1100
 ctgagtccag cagacctcc agtggggcca gcacagccac caactctgag 1150
 tccagcacga cctccagtgg ggctagcaca gccaccaact ctgactccag 1200
 cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag 1250
 tgtccagtgg gatcagcaca gtcaccaatt ctgagtccag cacacctcc 1300
 agtggggcca acacagccac caactctgag tccagtacga cctccagtgg 1350
 ggccaacaca gccaccaact ctgagtccag cacagtgtcc agtggggcca 1400
 gcaactgccac caactctgag tccagcaca cctccagtgg ggtcagcaca 1450
 gccaccaact ctgagtccag cacaacctcc agtggggcta gcacagccac 1500

caactctgac tccagcacia cctccagtga ggccagcaca gccaccaact 1550
 ctgagtctag cacagtgtcc agtgggatca gcacagtcac caattctgag 1600
 tccagcacia cctccagtgg ggccaacaca gccaccaact ctgggtccag 1650
 tgtgacctct gcaggctctg gaacagcagc tctgactgga atgcacacaa 1700
 cttcccatag tgcattctact gcagtgagtg aggcaaagcc tgggtgggtcc 1750
 ctgggtgccgt gggaaatctt cctcatcacc ctgggtctcgg ttgtggcggc 1800
 cgtggggctc tttgctgggc tcttcttctg tgtgagaaac agcctgtccc 1850
 tgagaaacac ctttaacaca gctgtctacc accctcatgg cctcaacat 1900
 ggcccttggtc caggcccttg aggaatcat ggagcccccc acaggcccag 1950
 gtggagtcct aactggttct ggaggagacc agtatcatcg atagccatgg 2000
 agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgcc 2050
 gcattcttca ggaaggaaga gacctgggca cccaagacct ggtttctttt 2100
 cattcatccc aggagacccc tcccagcttt gtttgagatc ctgaaaatct 2150
 tgaagaaggt attcctcacc tttcttgctt ttaccagaca ctggaaagag 2200
 aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250
 acacgacaaa gagaagctgt gcttgccccg ggtggtgtat ctagctctga 2300
 gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350
 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
1				5					10					15
Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20					25					30
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35					40					45
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50					55					60
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65					70					75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	
				80					85					90	
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	
				95					100					105	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				110					115					120	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	
				125					130					135	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				140					145					150	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				155					160					165	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				170					175					180	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				185					190					195	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				200					205					210	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				215					220					225	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				230					235					240	
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	
				245					250					255	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				260					265					270	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				275					280					285	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				290					295					300	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				305					310					315	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	
				320					325					330	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	
				335					340					345	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	
				350					355					360	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	

	365		370		375
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr	Ala		
	380	385	390		
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Val Ser Thr	Ala		
	395	400	405		
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala		
	410	415	420		
Thr Asn Ser Asp	Ser Ser Thr Thr Ser	Ser Glu Ala Ser Thr	Ala		
	425	430	435		
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr	Val		
	440	445	450		
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr	Ala		
	455	460	465		
Thr Asn Ser Gly	Ser Ser Val Thr Ser	Ala Gly Ser Gly Thr	Ala		
	470	475	480		
Ala Leu Thr Gly	Met His Thr Thr Ser	His Ser Ala Ser Thr	Ala		
	485	490	495		
Val Ser Glu Ala	Lys Pro Gly Gly Ser	Leu Val Pro Trp Glu	Ile		
	500	505	510		
Phe Leu Ile Thr	Leu Val Ser Val Val	Ala Ala Val Gly Leu	Phe		
	515	520	525		
Ala Gly Leu Phe	Phe Cys Val Arg Asn	Ser Leu Ser Leu Arg	Asn		
	530	535	540		
Thr Phe Asn Thr	Ala Val Tyr His Pro	His Gly Leu Asn His	Gly		
	545	550	555		
Leu Gly Pro Gly	Pro Gly Gly Asn His	Gly Ala Pro His Arg	Pro		
	560	565	570		
Arg Trp Ser Pro	Asn Trp Phe Trp Arg	Arg Pro Val Ser Ser	Ile		
	575	580	585		
Ala Met Glu Met	Ser Gly Arg Asn Ser	Gly Pro			
	590	595			

<210> 244
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50

ttcccgaacct tcccagcaat atgcatcttg cacgtctggc cggtcctgc 100

tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150

ccccattgag aaggtcattg aagggatcaa ccgaggggctg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400

gaagcagaga agcttgGCCa tggggTcaac aacgctgctg gacaggccgg 450

gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500

ctgggaagga agcagagaaa cttggccaag gggTcaacca tgctgctgac 550

caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650
 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700
 tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750
 agtcaacacg cctttcatca accttccgc cctgtggagg agcgtcgcca 800
 acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850
 gttgtcacat cagctgacat gacctggagg gggtgggggt gggggacagg 900
 tttctgaaat ccctgaaggg gggtgtactg ggatttgtga ataaacttga 950
 tacacca 957

<210> 248
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly
215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
230 235 240

Ser Val Ala Asn Ile Met Pro
245

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcat cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttcctttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgacccatt gagaaggatca ttgaaggat caaccgagg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252

ctccgggtcc ccaggggctg cgccgggccc gcctggcaag ggggacgagt 50
cagtggacac tccaggaaga gcggccccgc ggggggcgat gaccgtgcgc 100
tgaccctgac tcaactccagg tccggaggcg ggggcccccg gggcgactcg 150
ggggcggacc gcgggggcga gctgccgccc gtgagtccgg ccgagccacc 200
tgagcccag cgcggggaca ccgtcgctcc tgctctccga atgctgcgca 250
ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 300
cctcggccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc 350
gccgcctccg acctgggcgc tcagcccccg gatcagcctg cctctgggct 400
ctgaagagcg gccattcctc agattcgaag ctgaacacat ctccaactac 450
acagcccttc tgctgagcag ggatggcagg accctgtacg tgggtgctcg 500
agaggccctc tttgcaactca gtagcaacct cagcttcctg ccaggcgggg 550
agtaccagga gctgctttgg ggtgcagacg cagagaagaa acagcagtgc 600
agcttcaagg gcaaggaccc acagcgcgac tgtcaaaact acatcaagat 650
cctcctgccg ctacgcggca gtcacctgtt cacctgtggc acagcagcct 700
tcagccccat gtgtacctac atcaacatgg agaacttcac cctggcaagg 750
gacgagaagg ggaatgtcct cctggaagat ggcaagggcc gttgtccctt 800
cgaccgcaat ttcaagtcca ctgccctggg ggttgatggc gagctctaca 850
ctggaacagt cagcagcttc caagggaatg acccggccat ctgcgggagc 900
caaagccttc gccccaccaa gaccgagagc tccctcaact ggctgcaaga 950
cccagctttt gtggcctcag cctacattcc tgagagcctg ggagccttgc 1000
aaggcgatga tgacaagatc tactttttct tcagcgagac tggccaggaa 1050
tttgagttct ttgagaacac cattgtgtcc cgcattgccg gcattctgaa 1100
gggcgatgag ggtggagagc ggggtgtaca gcagcgctgg acctccttcc 1150
tcaaggccca gctgctgtgc tcacggcccg acgatggctt ccccttcaac 1200
gtgctgcagg atgtcttcac gctgagcccc agccccagg actggcgtga 1250
cacccttttc tatggggtct tcaactccca gtggcacagg ggaactacag 1300
aaggctctgc cgtctgtgtc ttcacaatga aggatgtgca gagagtcttc 1350
agcggcctct acaaggaggt gaaccgtgag acacagcagt ggtacaccgt 1400
gaccaccccg gtgcccacac cccggcctgg agcgtgcac accaacagt 1450

cccgggaaag gaagatcaac tcatccctgc agctcccaga ccgcgtgctg 1500
 aacttcctca aggaccactt cctgatggac gggcaggtcc gaagccgcat 1550
 gctgctgctg cagccccagg ctgctacca gcgcgtggct gtacaccgag 1600
 tccctggcct gcaccacacc tacgatgtcc tcttcctggg cactggtgac 1650
 ggccggctcc acaaggcagt gagcgtgggc ccccggtgc acatcattga 1700
 ggagctgcag atcttctcat cgggacagcc cgtgcagaat ctgctcctgg 1750
 acaccacag ggggctgctg tatgcggcct cacactcggg cgtagtccag 1800
 gtgcccattg ccaactgcag cctgtaccgg agctgtgggg actgcctcct 1850
 cgccgggac ccctactgtg cttggagcgg ctccagctgc aagcacgtca 1900
 gcctctacca gcctcagctg gccaccaggc cgtggatcca ggacatcgag 1950
 ggagccagcg ccaaggacct ttgcagcggg tcttcggttg tgtccccgtc 2000
 tttgtacca acaggggaga agccatgtga gcaagtccag ttccagcca 2050
 acacagtga cactttggcc tgcccgtcc tctccaacct ggcgaccga 2100
 ctctggctac gcaacggggc ccccgtaat gcctcggcct cctgccacgt 2150
 gctaccact ggggacctgc tgctgggtgg cacccaacag ctgggggagt 2200
 tccagtgtg gtactagag gagggcttcc agcagctggt agccagctac 2250
 tgcccagag tggtggagga cggggtggca gaccaaagc atgaggggtg 2300
 cagtgtaccc gtcattatca gcacatcgcg tgtgagtga ccagctggtg 2350
 gcaaggccag ctggggtgca gacaggctct actggaagga gttcctggtg 2400
 atgtgcacgc tctttgtgct ggccgtgctg ctcccagttt tattcttgct 2450
 ctaccggcac cggaacagca tgaaagtctt cctgaagcag ggggaatgtg 2500
 ccagcgtgca cccaagacc tgccctgtgg tgctgcccc tgagaccgc 2550
 ccactcaacg gcctagggcc ccctagcacc ccgctcgatc accgagggta 2600
 ccagtcctg tcagacagcc ccccgggggc ccgagctctc actgagtcag 2650
 agaagaggcc actcagcatc caagacagct tcgtggaggt atccccagt 2700
 tgccccggc cccgggtccg ccttggtcgt gagatccgtg actctgtggt 2750
 gtgagagctg acttccagag gacgtgccc tggttcagg ggctgtgaat 2800
 gctcgagag ggtcaactgg acctcccctc cgctctgctc ttctgtgaac 2850
 acgaccgtg tgcccgccc ttgggagcct tggagccagc tggcctgctg 2900

ctctccagtc aagtagcgaa gctcctacca cccagacacc caaacagccg 2950
 tggccccaga ggtcctggcc aaatatgggg gcctgcctag gttggtggaa 3000
 cagtgtcctt tatgtaaact gagccctttg tttaaaaaac aattccaaat 3050
 gtgaaactag aatgagaggg aagagatagc atggcatgca gcacacacgg 3100
 ctgctccagt tcatggcctc ccaggggtgc tggggatgca tccaaagtgg 3150
 ttgtctgaga cagagttgga aaccctcacc aactggcctc ttcaccttcc 3200
 acattatccc gctgccaccg gctgccctgt ctactgcag attcaggacc 3250
 agcttgggct gcgtgcgttc tgccttgcca gtcagccgag gatgtagttg 3300
 ttgctgccgt cgtcccacca cctcaggga cagagggcta ggttggcact 3350
 gcggccctca ccaggtcctg ggctcggacc caactcctgg acctttccag 3400
 cctgtatcag gctgtggcca cacgagagga cagcgcgagc tcaggagaga 3450
 tttcgtgaca atgtacgcct ttccctcaga attcaggga gagactgtcg 3500
 cctgccttcc tccgttgttg cgtgagaacc cgtgtgcccc ttcccacat 3550
 atccaccctc gctccatctt tgaactcaaa cacgaggaac taactgcacc 3600
 ctggtcctct cccagtcctc cagttcacc tccatccctc accttccctc 3650
 actctaaggg atatcaacac tgcccagcac agggggccctg aatttatgtg 3700
 gtttttatac attttttaat aagatgcact ttatgtcatt ttttaataaa 3750
 gtctgaagaa ttactgttta aaaaaaaaaa a 3781

<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

Met	Leu	Arg	Thr	Ala	Met	Gly	Leu	Arg	Ser	Trp	Leu	Ala	Ala	Pro
1				5					10					15
Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu

80										85					90				
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr					
				95					100					105					
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys					
				110					115					120					
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile					
				125					130					135					
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly					
				140					145					150					
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn					
				155					160					165					
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp					
				170					175					180					
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala					
				185					190					195					
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe					
				200					205					210					
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro					
				215					220					225					
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe					
				230					235					240					
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly					
				245					250					255					
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu					
				260					265					270					
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile					
				275					280					285					
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp					
				290					295					300					
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp					
				305					310					315					
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro					
				320					325					330					
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr					
				335					340					345					
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val					
				350					355					360					
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys					
				365					370					375					

Glu Val Asn Arg	Glu Thr Gln Gln Trp	Tyr Thr Val Thr His Pro	380	385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys	Ile Thr Asn Ser Ala Arg	395	400	405
Glu Arg Lys Ile	Asn Ser Ser Leu Gln	Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys	Asp His Phe Leu Met	Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val	Pro Gly Leu His His	Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His	Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His	Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp	Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser	His Ser Gly Val Val	Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser	Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser	Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser	Cys His Val Leu Pro	Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu Glu	650	655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser	Tyr Cys Pro Glu Val Val			

665					670					675				
Glu	Asp	Gly	Val	Ala	Asp	Gln	Thr	Asp	Glu	Gly	Gly	Ser	Val	Pro
				680					685					690
Val	Ile	Ile	Ser	Thr	Ser	Arg	Val	Ser	Ala	Pro	Ala	Gly	Gly	Lys
				695					700					705
Ala	Ser	Trp	Gly	Ala	Asp	Arg	Ser	Tyr	Trp	Lys	Glu	Phe	Leu	Val
				710					715					720
Met	Cys	Thr	Leu	Phe	Val	Leu	Ala	Val	Leu	Leu	Pro	Val	Leu	Phe
				725					730					735
Leu	Leu	Tyr	Arg	His	Arg	Asn	Ser	Met	Lys	Val	Phe	Leu	Lys	Gln
				740					745					750
Gly	Glu	Cys	Ala	Ser	Val	His	Pro	Lys	Thr	Cys	Pro	Val	Val	Leu
				755					760					765
Pro	Pro	Glu	Thr	Arg	Pro	Leu	Asn	Gly	Leu	Gly	Pro	Pro	Ser	Thr
				770					775					780
Pro	Leu	Asp	His	Arg	Gly	Tyr	Gln	Ser	Leu	Ser	Asp	Ser	Pro	Pro
				785					790					795
Gly	Ala	Arg	Val	Phe	Thr	Glu	Ser	Glu	Lys	Arg	Pro	Leu	Ser	Ile
				800					805					810
Gln	Asp	Ser	Phe	Val	Glu	Val	Ser	Pro	Val	Cys	Pro	Arg	Pro	Arg
				815					820					825
Val	Arg	Leu	Gly	Ser	Glu	Ile	Arg	Asp	Ser	Val	Val			
				830					835					

<210> 254
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 254
 agcccggtgca gaatctgctc ctgg 24

<210> 255
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 255
 tgaagccagg gcagcgctcct ctgg 24

<210> 256
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 256
 gtacaggctg cagttggc 18

<210> 257
 <211> 41
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-41
 <223> Synthetic construct.

<400> 257
 agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 258
 gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259
 <211> 4563
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 3635
 <223> unknown base

<400> 259
 ctaagccgga ggatgtgcag ctgcggcggc ggcgccggct acgaagagga 50
 cggggacagg cgccgtgcga accgagccca gccagccgga ggacgcgggc 100
 agggcggggac gggagcccg actcgtctgc cgccgccgtc gtcgccgtcg 150

tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200
 cgcccagacc gccgctagcg cgcgccgggc atgggtcccct cttaaaggcg 250
 caggccgcgg cggcgggggc ggggtgtgcgg aacaaagcgc cggcgcgggg 300
 cctgcggggc gctcgggggc cgcgatgggc gcggcgggcc cgcggcggcg 350
 gcggcgctgc ccgggccggg cctcgcggcg ctagggcggg ctggcctccg 400
 tgggcggggg cagcgggctg agggcgcgcg gaggctgcgg cggcggcggc 450
 ggcggcggcg gcggccccgc gggcgagcgg gcgcgggcat ggccgcgcgc 500
 ggccggcgcg cctggctcag cgtgctgctc gggctcgtcc tgggcttcgt 550
 gctggcctcg cggtcgtcc tgccccgggc ttccgagctg aagcgagcgg 600
 gcccacggcg ccgcgccagc cccgagggct gccggtccgg gcaggcggcg 650
 gcttcccagg ccggcggggc gcgcggcgat gcgcgcgggg cgcagctctg 700
 gccgccccgc tcggacccag atggcggccc gcgcgacagg aactttctct 750
 tcgtgggagt catgaccgcc cagaaatacc tgcagactcg ggccgtggcc 800
 gcctacagaa catggtccaa gacaattcct gggaaagttc agttcttctc 850
 aagtgagggg tctgacacat ctgtaccaat tccagtagtg ccactacggg 900
 gtgtggacga ctctacccg cccagaaga agtccttcat gatgctcaag 950
 tacatgcacg accactactt ggacaagtat gaatggttta tgagagcaga 1000
 tgatgacgtg tacatcaaag gagaccgtct ggagaacttc ctgaggagtt 1050
 tgaacagcag cgagccccctc tttcttgggc agacaggcct gggcaccacg 1100
 gaagaaatgg gaaaactggc cctggagcct ggtgagaact tctgcatggg 1150
 ggggcctggc gtgatcatga gccgggaggt gcttcggaga atggtgccgc 1200
 acattggcaa gtgtctccgg gagatgtaca ccacccatga ggacgtggag 1250
 gtgggaagggt gtgtccggag gtttgcaggg gtgcagtgtg tctggtctta 1300
 tgagatgcgg cagctttttt atgagaatta cgagcagaac aaaaaggggt 1350
 acattagaga tctccataac agtaaaattc accaagctat cacattacac 1400
 cccaacaaaa acccacccta ccagtacagg ctccacagct acatgctgag 1450
 ccgcaagata tccgagctcc gccatcgcac aatacagctg caccgcgaaa 1500
 ttgtcctgat gagcaaatac agcaacacag aaattcataa agaggacctc 1550
 cagctgggaa tccctccctc cttcatgagg tttcagcccc gccagcgaga 1600

ggagattctg gaatgggagt ttctgactgg aaaatacttg tattcggcag 1650
 ttgacggcca gcccctcga agaggaatgg actccgcca gaggaagcc 1700
 ttggacgaca ttgtcatgca ggtcatggag atgatcaatg ccaacgcaa 1750
 gaccagaggg cgcattcattg acttcaaaga gatccagtac ggctaccgcc 1800
 gggatgaacc catgtatggg gctgagtaca tcctggacct gctgcttctg 1850
 tacaaaaagc acaaaggga gaaaatgacg gtccctgtga ggaggcacgc 1900
 gtatttacag cagactttca gcaaaatcca gtttgtggag catgaggagc 1950
 tggatgcaca agagttggcc aagagaatca atcaggaatc tggatccttg 2000
 tcctttctct caaactccct gaagaagctc gtcccctttc agctccctgg 2050
 gtcgaagagt gagcacaag aacccaaaga taaaagata aacatactga 2100
 ttcctttgtc tgggcgtttc gacatgtttg tgagatttat gggaaacttt 2150
 gagaagacgt gtcttatccc caatcagaac gtcaagctcg tggttctgct 2200
 tttcaattct gactccaacc ctgacaaggc caaacaagtt gaactgatga 2250
 gagattaccg cattaagtag cctaaagccg acatgcagat tttgctgtg 2300
 tctggagagt tttcaagagc cctggccctg gaagtaggat cctcccagtt 2350
 taacaatgaa tctttgctct tcttctgcga cgtcgacctc gtgtttacta 2400
 cagaattcct tcagcgatgt cgagcaaata cagttctggg ccaacaata 2450
 tattttccaa tcatcttcag ccagtatgac ccaaagattg tttatagtgg 2500
 gaaagttccc agtgacaacc attttgcctt tactcagaaa actggcttct 2550
 ggagaaacta tgggtttggc atcacgtgta tttataaggg agatcttgtc 2600
 cgagtgggtg gctttgatgt ttccatccaa ggctgggggc tggaggatgt 2650
 ggaccttttc aacaaggttg tccaggcagg tttgaagacg tttaggagcc 2700
 aggaagtagg agtagtccac gtccaccatc ctgtcttttg tgatcccaat 2750
 cttgacccca aacagtacaa aatgtgcttg ggggccaaag catcgacctc 2800
 tgggtccacc cagcagctgg ctgagatgtg gctggaaaaa aatgatccaa 2850
 gttacagtaa aagcagcaat aataatggct cagtgaggac agcctaattg 2900
 ccagctttgc tggaaaagac gtttttaatt atctaattta tttttcaaaa 2950
 attttttgta tgatcagttt ttgaagtccg tatacaagga tatattttac 3000
 aagtggtttt cttacatagg actcctttaa gattgagctt tctgaacaag 3050

aaggatgatca gtgtttgcct ttgaacacat cttcttgctg aacattatgt 3100
agcagacctg cttactttg acttgaaatg tacctgatga acaaaacttt 3150
tttaaaaaaa tgttttcttt tgagaccctt tgctccagtc ctatggcaga 3200
aaacgtgaac attcctgcaa agtattattg taacaaaaca ctgtaactct 3250
ggtaaagtgt ctgttgatg tgtaacatt ccacagattc taccttttgt 3300
gttttgttt ttttttttac aattgtttta aagccatttc atgttccagt 3350
tgtaagataa ggaaatgtga taatagctgt ttcattcattg tcttcaggag 3400
agctttccag agttgatcat ttcctctcat ggtactctgc tcagcatggc 3450
cacgtagggt ttttgtttgt tttgttttgt tctttttttg agacggagtc 3500
tcactctgtt acccaggctg gaatgcagtg gcgcaatctt ggctcacttt 3550
aacctccact tccctgggtc aagcaattcc cctgcctttg cctcccaggt 3600
agctgggatt acaggcacac accaccacgc ccagntagtt tttttgtatt 3650
tttagtagag acgggggttc accatgcaag ccagctggc cacgtagggt 3700
ttaagcaag gggcgtgaag aaggcacagt gaggtatgtg gctgttctcg 3750
tggtagtcca ttcggcctaa atagacctgg cattaaattt caagaaggat 3800
ttggcatttt ctcttcttga cccttctctt taaagggtaa aatattaatg 3850
tttagaatga caaagatgaa ttattacaat aaatctgatg tacacagact 3900
gaaacataca cacatacacc ctaatcaaaa cggtggggaa aaatgtattt 3950
ggttttgttc ctttcatcct gtctgtgtta tgtgggtgga gatggttttc 4000
attctttcat tactgttttg ttttatcctt tgtatctgaa ataccttta 4050
tttatttaat atctgttgtt cagagctctg ccatttcttg agtacctgtt 4100
agttagtatt atttatgtgt atcgggagtg tgtttagtct gttttatttg 4150
cagtaaaccg atctccaaag atttcctttt ggaaacgctt tttccctcc 4200
ttaattttta tattccttac tgttttacta aatattaagt gttctttgac 4250
aattttggtg ctcatgtgtt ttggggacaa aagtgaaatg aatctgtcat 4300
tataccagaa agttaaattc tcagatcaaa tgtgccttaa taaatttggt 4350
ttcattttaga ttcaaacag tgatagactt gccattttta tacacgtcat 4400
tgaggaggctg cgtatttgta aatagcctga tgctcatttg gaaaaataaa 4450
ccagtgaaca atatttttct attgtacttt tcgaaccatt ttgtctcatt 4500

attcctgttt tagctgaaga attgtattac atttggagag taaaaaactt 4550

aaacacgaaa aaa 4563

<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

Met	Ala	Ala	Arg	Gly	Arg	Arg	Ala	Trp	Leu	Ser	Val	Leu	Leu	Gly	
1				5					10					15	
Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg	
				20					25					30	
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro	
				35					40					45	
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	
				50					55					60	
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	
				65					70					75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	
				80					85					90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	
				95					100					105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	
				110					115					120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	
				125					130					135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	
				140					145					150	
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	
				155					160					165	
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	
				170					175					180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	
				185					190					195	
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	
				200					205					210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	
				215					220					225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	
				230					235					240	

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

530					535					540				
Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg	Phe	Met	Gly	Asn	Phe	Glu
				545					550					555
Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu
				560					565					570
Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp	Lys	Ala	Lys	Gln	Val	Glu
				575					580					585
Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln
				590					595					600
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu
				605					610					615
Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys
				620					625					630
Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg
				635					640					645
Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe
				650					655					660
Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser
				665					670					675
Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn
				680					685					690
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg
				695					700					705
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp
				710					715					720
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe
				725					730					735
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe
				740					745					750
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly
				755					760					765
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met
				770					775					780
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn
				785					790					795
Asn	Gly	Ser	Val	Arg	Thr	Ala								
				800										

<210> 261

<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatTTct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
ggacaaccgt tgctgggtgt cccagggcct gaggcaggac ggtactccgc 50
tgacaccttc cctttcggcc ttgaggttcc cagcctggtg gccccaggac 100
gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150
tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450
 gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccacattc 500
 tggtcgatca aaccaaacaa tgtttccatt gttttgcatg cagaggaacc 550
 ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaaac 600
 aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650
 ccatatgtta cctcatacaa gtcacctgtc accactttag ataagagcac 700
 tggcattgag atctctacag aatcagaaga tggtcctcag ctctcaggtg 750
 aaactgcatg agaaaaaccc gaagagtttg gaaagcaccc agagagttgg 800
 aataatgatg acattttgaa aaaaatttta gatattaatt cacaagtgca 850
 acaggcactt cttagtgaac ccagcaaccc agcatataga gaagatattg 900
 aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950
 gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000
 aacaagtaat aaaattgatg acatcgaaac tggtattaac atgctgtgta 1050
 attctagatc taaactctat gaatatttag atattaaatg tgttccacca 1100
 gagatgagag aaaaagctgc tacagtattc aatacattaa aaaatatgtg 1150
 tagatcaagg agagtcacag cttattataa agtttattaa acaataatat 1200
 aaaaatttta aacctacttg atattccata acaaagctga ttttaagcaaa 1250
 ctgcattttt tcacaggaga aataatcata ttcgtaattt caaaagttgt 1300
 ataaaaatat tttctattgt agttcaaagtg tgccaacatc tttatgtgtc 1350
 atgtgttatg aacaattttc atatgcacta aaaaccta ataaaaataa 1400
 attttggttc aggaaaaaa 1419

<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
1				5					10					15

Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50										55					60				
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys					
				65					70					75					
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu					
				80					85					90					
Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly					
				95					100					105					
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro					
				110					115					120					
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala					
				125					130					135					
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu					
				140					145					150					
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val					
				155					160					165					
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro					
				170					175					180					
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu					
				185					190					195					
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys					
				200					205					210					
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp					
				215					220					225					
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala					
				230					235					240					
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu					
				245					250					255					
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala					
				260					265					270					
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro					
				275					280					285					
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile					
				290					295					300					
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp					
				305					310					315					
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val					
				320					325					330					
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala					
				335					340					345					

Leu Leu Lys Val Tyr
350

<210> 266
<211> 2403
<212> DNA
<213> Homo sapiens

<400> 266
cggctcgagc ggctcgagt aagagcctct ccacggctcc tgcgcctgag 50
acagctggcc tgacctcaa atcatccatc caccctgct gtcctctgtt 100
ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150
tttggttctc agtttctacg agctggtgtc aggacagtgg caagtcactg 200
gaccgggcaa gtttgtccag gccttgggtg gggaggacgc cgtgttctcc 250
tgctccctct ttcctgagac cagtgcagag gctatggaag tgcggttctt 300
caggaatcag ttccatgctg tggccacct ctacagagat ggggaagact 350
gggaatctaa gcagatgcca cagtatcgag ggagaactga gtttgtgaag 400
gactccattg caggggggcg tgtctctcta aggctaaaaa acatcactcc 450
ctcggacatc ggcctgtatg ggtgctggtt cagttcccag atttactgat 500
aggaggccac ctgggagctg cgggtggcag cactgggctc acttcctctc 550
atttccatcg tgggatatgt tgacggaggt atccagttac tctgctgtc 600
ctcaggctgg tttccccagc ccacagccaa gtggaaaggc ccacaaggac 650
aggatttgtc ttcagactcc agagcaaagt cagatgggta cagcctgtat 700
gatgtggaga tctccattat agtccaggaa aatgctggga gcatattgtg 750
ttccatccac ctgctgagc agagtcatga ggtggaatcc aaggtattga 800
taggagagac gttttccag ccctcacctt ggcgcctggc ttctatttta 850
ctcgggttac tctgtggtgc cctgtgtggt gttgtcatgg ggatgataat 900
tgttttcttc aaatccaaag ggaaaatcca ggcggaactg gactggagaa 950
gaaagcacgg acaggcagaa ttgagagacg cccggaaaca cgagtgag 1000
gtgactctgg atccagagac ggctcaccgc aagctctgcg tttctgatct 1050
gaaaactgta acccatagaa aagctcccca ggaggtgcct cactctgaga 1100
agagatttac aaggaagagt gtggtggctt ctcagggttt ccaagcaggg 1150
agacattact gggaggtgga cgtgggacaa aatgtagggt ggtatgtggg 1200
agtgtgtcgg gatgacgtag acagggggaa gaacaatgtg actttgtctc 1250

ccaacaatgg gtattgggtc ctgagactga caacagaaca tttgtatttc 1300
 acattcaatc cccatTTTTat cagcctcccc cccagcaccc ctcttacacg 1350
 agtaggggtc ttcctggact atgaggggtg gaccatctcc ttcttcaata 1400
 caaatgacca gtcccttatt tataccctgc tgacatgtca gtttgaaggc 1450
 ttgttgagac cctatatcca gcatgcgatg tatgacgagg aaaaggggac 1500
 tcccatattc atatgtccag tgtcctgggg atgagacaga gaagaccctg 1550
 cttaaagggc cccacaccac agaccagac acagccaagg gagagtgtc 1600
 ccgacaggtg gccccagctt cctctccgga gcctgcgcac agagagtcac 1650
 gccccctact ctctttagg gagctgaggt tcttctgccc tgagccctgc 1700
 agcagcggca gtcacagctt ccagatgagg ggggattggc ctgaccctgt 1750
 gggagtcaga agccatggct gccctgaagt ggggacggaa tagactcaca 1800
 ttaggttttag tttgtgaaaa ctccatccag ctaagcgatc ttgaacaagt 1850
 cacaacctcc caggctcctc atttgctagt cacggacagt gattcctgcc 1900
 tcacaggtga agattaaaga gacaacgaat gtgaatcatg cttgcagggt 1950
 tgagggcaca gtgtttgcta atgatgtgtt tttatattat acattttccc 2000
 accataaact ctgtttgctt attccacatt aatttacttt tctctatacc 2050
 aaatcaccca tggaatagtt attgaacacc tgctttgtga ggctcaaaga 2100
 ataaagagga ggtaggattt ttcactgatt ctataagccc agcattacct 2150
 gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200
 gtccatatcc ctcatataca cagacacaaa aattctaaat aaaattttta 2250
 caaattaaac taaacaatat atttaaagat gatataaac tactcagtgt 2300
 ggtttgtccc acaaatgcag agttgggtta atatttaa atcaaccagt 2350
 gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400
 aa 2403

<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

Met	Ala	Phe	Val	Leu	Ile	Leu	Val	Leu	Ser	Phe	Tyr	Glu	Leu	Val
1				5				10					15	

Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

20	25	30
Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu	35	40 45
Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe	50	55 60
His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser	65	70 75
Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp	80	85 90
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr	95	100 105
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile	110	115 120
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly	125	130 135
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile	140	145 150
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala	155	160 165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg	170	175 180
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile	185	190 195
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu	200	205 210
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu	215	220 225
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu	230	235 240
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile	245	250 255
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp	260	265 270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys	275	280 285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys	290	295 300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro	305	310 315

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	325	330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

Gly

<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
 ccttcacagg actcttcatt gctgggtggc aatgatgtat cggccagatg 50
 tggtagaggc taggaaaaga gtttggtggg aaccctgggt tatcggcctc 100
 gtcattctca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
 tgtcattttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
 attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350
 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
 agatttcact ctactgagga tctgaaact gtagataaaa ttgttcaact 450
 tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

ctactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550
 ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
 caggatcggt ggtgggacag aagtagaaga gggatgaatgg ccctggcagg 650
 ctagcctgca gtgggatggg agtcatcgct gtggagcaac cttaattaat 700
 gccacatggc ttgtgagtgc tgctcactgt tttacaacat ataagaaccc 750
 tgccagatgg actgcttcct ttggagtaac aataaaacct tcgaaaatga 800
 aacggggctc ccggagaata attgtccatg aaaaatacaa acacccatca 850
 catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900
 aaatgcagta catagagttt gtctccctga tgcacccat gagtttcaac 950
 caggatgatg gatgtttgtg acaggatttg gagcactgaa aaatgatgg 1000
 tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050
 aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100
 tatgtgctgg ctcccttagaa ggaaaaacag atgcatgcca gggatgactc 1150
 ggaggaccac tggtagttc agatgctaga gatatctgg accttgctgg 1200
 aatagtgagc tggggagatg aatgtgcaa acccaacaag cctgggtgtt 1250
 atactagagt tacggccttg cgggactgga ttacttcaaa aactggatc 1300
 taagagacaa aagcctcatg gaacagataa catTTTTTTT tgtTTTTTgg 1350
 gtgtggaggc catTTTTTga gatacagaat tggagaagac ttgcaaaaca 1400
 gctagatttg actgatctca ataaactgtt tgcttgatgc atgtattttc 1450
 ttccagctc tgtccgcac gtaagcatcc tgcttctgcc agatcaactc 1500
 tgtcatctgt gagcaatagt tgaaacttta tgtacataga gaaatagata 1550
 atacaatatt acattacagc ctgtattcat ttgttctcta gaagttttgt 1600
 cagaattttg acttgttgac ataaatttgt aatgcatata tacaatttga 1650
 agcactcctt ttcttcagtt cctcagctcc tctcatttca gcaaatatcc 1700
 attttcaagg tgacagaaca ggagtgaag aaaatataag aagaaaaaaa 1750
 tcccctacat ttatttgga cagaaaagta ttaggtgtt ttcttagtgg 1800
 aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850
 aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900
 tccagaaaga agccaagata tatccttatt ttcatttcca aacaactact 1950

atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050
 ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100
 cca 2103

<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269
 Met Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys
 1 5 10 15
 Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile
 20 25 30
 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35 40 45
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95 100 105
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
 110 115 120
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
 125 130 135
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
 155 160 165
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
 170 175 180
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
 200 205 210
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
 215 220 225

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro
				230					235					240
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys
				245					250					255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys
				260					265					270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser
				275					280					285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
				290					295					300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly
				305					310					315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
				320					325					330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
				335					340					345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
				350					355					360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
				365					370					375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
				380					385					390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
				395					400					405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys
				410					415					420

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

```

gtcgaaggtt ataaaagctt ccagccaaac ggcattgaag ttgaagatac 50
aacctgacag cacagcctga gatcttgggg atccctcagc ctaacaccca 100
cagacgtcag ctggtggatt cccgctgcat caaggcctac ccactgtctc 150
catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200
ttcccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250

```

gatgagactg agacggcgtg gccgcctttg cgggctgtcc cctgcgacta 300
 cgaccactgc cgacacctgc aggtgccctg caaggagcta cagagggtcg 350
 ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400
 gacccgccgc gcatgggaga agtgcgcatg gcggccgaag agggccgcgc 450
 agtgggtccac tgggtgtgccc cttctctccc ggctctccac tactggctgc 500
 tgctttggga cggcagcgag gctgcgcaga aggggcccc gctgaacgct 550
 acgggtccga gagccgaact gaaggggctg aagccagggg gcatttatgt 600
 cgtttgcgta gtggccgcta acgaggccgg ggcaagccgc gtgccccagg 650
 ctggaggaga gggcctcgag ggggcccaca tccctgcctt cgggccttgc 700
 agccgccttg cggtgccgcc caacccccgc actctggtcc acgcggccgt 750
 cggggtgggc acggccctgg cctgctaag ctgtgccgcc ctggtgtggc 800
 acttctgcct gcgcatcgc tggggctgcc cgcgccgagc cgccgcccga 850
 gccgcagggg cgctctgaaa ggggcctggg ggcctctcgg gcacagacag 900
 cccacactgg ggcgctcagc ctggcccccg ggaaagagga aaaccgctg 950
 cctccaggga gggctggacg gcgagctggg agccagcccc aggtccagg 1000
 gccacggcgg agtcatggtt ctcaggactg agcgcttggt taggtccggt 1050
 acttggcgct ttgtttcctg gctgaggtct gggaaggaat agaaaggggc 1100
 cccaatttt tttttaagcg gccagataat aaataatgta acctttgcgg 1150
 ttaaaaaaaaa aaaaaaaaaa 1170

<210> 271
 <211> 238
 <212> PRT
 <213> Homo sapiens

<400> 271
 Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe
 1 5 10 15
 Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu
 20 25 30
 Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
 35 40 45
 Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
 50 55 60
 Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
 65 70 75

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
				80					85					90	
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
			95						100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
			110						115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
			125						130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
			140						145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
			155						160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
			170						175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
			185						190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
			200						205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
			215						220					225	
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
			230						235						

<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

```

agagaaagaa gcgtctccag ctgaagccaa tgcagccctc cggtctctccg 50
cgaagaagtt ccctgccccg atgagcccc gccgtgcgtc cccgactatc 100
cccaggcggg cgtggggcac cgggcccagc gccgacgatc gctgccgttt 150
tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250
acgccctcaa tctgctcttt tggttaatgt ccatcagtgt gttggcagtt 300
tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga 350
aacgagggta gaggaagcag tcattttgac ttactttcct gtggttcatc 400
cggatcatgat tgctgtttgc tgtttcotta tcattgtggg gatgttagga 450
tattgtggaa cggtgaaaag aaatctgttg cttcttgcac ggtactttgg 500

```

aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttggacat 550
atgaacagga acttatgggt ccagtacaat ggtcagatat ggtcactttg 600
aaagccagga tgacaaatta tggattacct agatatcggg ggcttactca 650
tgcttggaaat ttttttcaga gagagtttaa gtgctgtgga gtagtatatt 700
tcaactgactg gttggaaatg acagagatgg actggccccc agattcctgc 750
tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct 800
cagtgaacctt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850
gaggaaccaa acaactgcag gtgctgaggt ttctgggaat ctccattggg 900
gtgacacaaa tcctggccat gattctcacc attactctgc tctgggctct 950
gtattatgat agaagggagc ctgggacaga ccaaatgatg tccttgaaga 1000
atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca 1050
agcctgtcaa gaatctttga acacacatcc atggcaaaca gctttaatac 1100
acactttgag atggaggagt tataaaaaga aatgtcacag aagaaaacca 1150
caaacttggt ttattggact tgtgaatttt tgagtacata ctatgtgttt 1200
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250
tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc 1300
accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat 1350
accactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg 1400
aggcagcatg gtttgattag catttccgca tccatgcaaa cgagtcacat 1450
atggtgggac tggagccata gtaaagggtg atttacttct accaactagt 1500
atataaagta ctaattaaat gctaacatag gaagttagaa aatactaata 1550
acttttatta ctacgcgac tattcttctg atgctaaata aattatatat 1600
cagaaaactt tcaatattgg tgactaccta aatgtgattt ttgctgggta 1650
ctaaaatatt cttaccactt aaaagagcaa gctaacacat tgtcttaagc 1700
tgatcagga ttttttgat ataagtctgt gttaaactctg tataattcag 1750
tcgatttcag ttctgataat gttaagaata accattatga aaaggaaaat 1800
ttgtcctgta tagcatcatt attttttagcc tttcctgtta ataaagcttt 1850
actattctgt cctgggctta tattacacat ataactgtta tttaaatact 1900
taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc 1950

agaatgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa 2000
 cttagttgat tcagaaagga cttgtatgct gtttttctcc caaatgaaga 2050
 ctctttttga cactaaacac tttttaaaaa gcttatcttt gccttctcca 2100
 aacaagaagc aatagtctcc aagtcaatat aaattctaca gaaaatagtg 2150
 ttctttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200
 tttagagatt ctttgtttta tttcactgat taatatactg tggcaaatta 2250
 cacagattat taaatTTTTT tacaagagta tagtatattt atttgaaatg 2300
 ggaaaagtgc attttactgt attttgtgta ttttgtttat ttctcagaat 2350
 atggaaagaa aattaaaatg tgtcaataaa tattttctag agagtaa 2397

<210> 273
 <211> 305
 <212> PRT
 <213> Homo sapiens

<400> 273
 Met Ala Arg Glu Asp Ser Val Lys Cys Leu Arg Cys Leu Leu Tyr
 1 5 10 15
 Ala Leu Asn Leu Leu Phe Trp Leu Met Ser Ile Ser Val Leu Ala
 20 25 30
 Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu
 35 40 45
 Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
 50 55 60
 Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
 65 70 75
 Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
 80 85 90
 Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
 95 100 105
 Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
 110 115 120
 Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met
 125 130 135
 Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp
 140 145 150
 Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe
 155 160 165
 Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser

170					175					180				
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln
				185					190					195
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met
				200					205					210
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe
				215					220					225
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu
				230					235					240
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro
				245					250					255
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His
				260					265					270
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg
				275					280					285
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe
				290					295					300
Glu	Met	Glu	Glu	Leu										
				305										

<210> 274
 <211> 2063
 <212> DNA
 <213> Homo sapiens

<400> 274
 gagagaggca gcagcttgct cagcggacaa ggatgctggg cgtgagggac 50
 caaggcctgc cctgcactcg ggcctcctcc agccagtgcg gaccagggac 100
 ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctctgctgc 150
 cttgggggtga caatctcagc tccaggctac agggagaccg ggaggatcac 200
 agagccagca tgttacagga tctgacagt gatcaacctc tgaacagcct 250
 cgatgtcaaa cccctgcgca aaccccgat ccccatggag accttcagaa 300
 aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350
 attgtggttg tctcatcaa ggtgattctg gataaatact acttctctg 400
 cgggcagcct ctccacttca tcccgaggaa gcagctgtgt gacggagagc 450
 tggactgtcc cttgggggag gacgaggagc actgtgtcaa gagcttcccc 500
 gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca 550
 ggtgctggac tcggccacag ggaactgggt ctctgcctgt ttcgacaact 600

tcacagaagc tctcgtgag acagcctgta ggcagatggg ctacagcaga 650
 gctgtggaga ttggcccaga ccaggatctg gatgttggtg aaatcacaga 700
 aaacagccag gagcttcgca tgcggaactc aagtgggccc tgtctctcag 750
 gctccctggt ctccctgcac tgtcttgctt gtgggaagag cctgaagacc 800
 ccccggtgtg tgggtgggga ggaggcctct gtggattctt ggccttggca 850
 ggtcagcatc cagtacgaca aacagcacgt ctgtggaggg agcatcctgg 900
 acccccactg ggtcctcacg gcagcccact gcttcaggaa acataccgat 950
 gtgttcaact ggaaggtgcg ggcaggctca gacaaactgg gcagcttccc 1000
 atccctggct gtggccaaga tcatcatcat tgaattcaac cccatgtacc 1050
 ccaaagacaa tgacatcgcc ctcatgaagc tgcagttccc actcactttc 1100
 tcaggcacag tcaggcccat ctgtctgccc ttctttgatg aggagctcac 1150
 tccagccacc ccactctgga tcattggatg gggctttacg aagcagaatg 1200
 gagggaaagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac 1250
 agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcaccgagaa 1300
 gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccaggggtg 1350
 acagtgggtg gccctgatg taccaatctg accagtggca tgtggtgggc 1400
 atcgtagct ggggctatg ctgcgggggc ccgagcacc caggagtata 1450
 caccaaggtc tcagcctatc tcaactggat ctacaatgtc tggaaggctg 1500
 agctgtaatg ctgtgcccc ttgacagtgc tgggagccgc ttccttctg 1550
 ccctgcccac ctggggatcc cccaaagtca gacacagagc aagagtcccc 1600
 ttgggtacac ccctctgccc acagcctcag catttcttgg agcagcaaag 1650
 ggcctcaatt cctgtaagag accctcgag cccagaggcg cccagaggaa 1700
 gtcagcagcc ctagctcggc cacacttggg gctcccagca tcccaggag 1750
 agacacagcc cactgaacaa ggtctcaggg gtattgctaa gccaagaagg 1800
 aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850
 tcaactgtgg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900
 tcttcacca tccccagcc tactagagca agaaaccagt tgtaataata 1950
 aatgcactgc cctactgttg gtatgactac cgttacctac tggtgtcatt 2000
 gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg 2050

caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met	Leu	Gln	Asp	Pro	Asp	Ser	Asp	Gln	Pro	Leu	Asn	Ser	Leu	Asp	
1				5					10					15	
Val	Lys	Pro	Leu	Arg	Lys	Pro	Arg	Ile	Pro	Met	Glu	Thr	Phe	Arg	
				20					25					30	
Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser	
				35					40					45	
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	
				50					55					60	
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	
				65					70					75	
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu	
				80					85					90	
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg	
				95					100					105	
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr	
				110					115					120	
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu	
				125					130					135	
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu	
				140					145					150	
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	
				155					160					165	
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser	
				170					175					180	
Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu	
				185					190					195	
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser	
				200					205					210	
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys	
				215					220					225	
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His	
				230					235					240	
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala	
				245					250					255	

Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys	260	265	270
Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp	275	280	285
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr	290	295	300
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro	305	310	315
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn	320	325	330
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val	335	340	345
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu	350	355	360
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val	365	370	375
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser	380	385	390
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys	395	400	405
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr	410	415	420
Leu	Asn	Trp	Ile	Tyr	Asn	Val	Trp	Lys	Ala	Glu	Leu				425	430	

<210> 276

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 276

```

gggctgaggc actgagagac cggaaagcct ggcattccag agggagggaa 50
acgcagcggc atccccaggc tccagagctc cctggtgaca gtctgtggct 100
gagcatggcc ctccagccc tgggcctgga cccctggagc ctccctgggcc 150
ttttcctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200
ggaggcgggc agggggccat gccaggggtc agatactatg caggggatga 250
acgtagggca cttagcttct tccaccagaa gggcctccag gattttgaca 300
ctctgctoct gagtgggtgat ggaaatactc tctacgtggg ggctcgagaa 350
gccattctgg ccttgatat ccaggatcca ggggtcccca ggctaaagaa 400

```

catgataccg tggccagcca gtgacagaaa aaagagtga tgtgccttta 450
agaagaagag caatgagaca cagtgtttca acttcatccg tgcctgggtt 500
tcttacaatg tcacccatct ctacacctgc ggcaccttcg ccttcagccc 550
tgcttgtagc ttcatgaac ttcaagattc ctacctgttg cccatctcgg 600
aggacaaggt catggaggga aaaggccaaa gcccctttga ccccgctcac 650
aagcataccg ctgtcttggt ggatgggatg ctctattctg gtactatgaa 700
caacttcctg ggcagtgagc ccatcctgat gcgcacactg ggatcccagc 750
ctgtcctcaa gaccgacaac ttctccgct ggctgcatca tgacgcctcc 800
tttgtggcag ccatcccttc gaccagggtc gtctacttct tcttcgagga 850
gacagccagc gagtttgact tctttgagag gctccacaca tcgcgggtgg 900
ctagagtctg caagaatgac gtgggcggcg aaaagctgct gcagaagaag 950
tggaccacct tcctgaaggc ccagctgctc tgcacccagc cggggcagct 1000
gcccttcaac gtcacccgac acgcgggtct gctccccgac gattctccca 1050
cagctcccca catctacgca gtcttcacct cccagtggca ggttggcggg 1100
accaggagct ctgcggtttg tgccttctct ctcttggaac ttgaacgtgt 1150
ctttaagggg aaatacaaag agttgaacaa agaaacttca cgctggacta 1200
cttatagggg ccctgagacc aacccccggc caggcagttg ctcagtgggc 1250
ccctcctctg ataaggccct gaccttcatg aaggaccatt tcctgatgga 1300
tgagcaagtg gtggggacgc ccctgctggt gaaatctggc gtggagtata 1350
cacggcttgc agtggagaca gcccagggcc ttgatgggca cagccatctt 1400
gtcatgtacc tgggaaccac cacagggtcg ctccacaagg ctgtggtaag 1450
tggggacagc agtgcctatc tgggtgaaga gattcagctg ttccctgacc 1500
ctgaacctgt tcgcaacctg cagctggccc ccacccaggg tgcagtgttt 1550
gtaggcttct caggaggtgt ctggagggtg ccccgagcca actgtagtgt 1600
ctatgagagc tgtgtggact gtgtccttgc ccgggacccc cactgtgcct 1650
gggaccctga gtcccgaacc tgttgcttcc tgtctgcccc caacctgaac 1700
tcctggaagc aggacatgga gcgggggaac ccagagtggg catgtgccag 1750
tggcccatg agcaggagcc ttcggcctca gagccgcccg caaatcatta 1800
aagaagtccct ggctgtcccc aactccatcc tggagctccc ctgccccac 1850

ctgtcagcct tggcctctta ttattggagt catggcccag cagcagtccc 1900
 agaagcctct tccactgtct acaatggctc cctcttgctg atagtgcagg 1950
 atggagttgg gggctcttac cagtgtggg caactgagaa tggcttttca 2000
 taccctgtga tctcctactg ggtggacagc caggaccaga ccctggccct 2050
 ggatcctgaa ctggcaggca tccccggga gcatgtgaag gtcccgttga 2100
 ccagggtcag tgggtggggc gccctggctg cccagcagtc ctactggccc 2150
 cactttgtca ctgtcactgt cctctttgcc ttagtgcttt caggagccct 2200
 catcatcctc gtggcctccc cattgagagc actccgggct cggggcaagg 2250
 ttcagggctg tgagaccctg cgcctgggg agaaggcccc gttaagcaga 2300
 gagcaacacc tccagtctcc caaggaatgc aggacctctg ccagtgatgt 2350
 ggacgctgac aacaactgcc taggcactga ggtagcttaa actctaggca 2400
 caggccgggg ctgcggtgca ggcacctggc catgctgggt gggcggccca 2450
 agcacagccc tgactaggat gacagcagca caaaagacca cctttctccc 2500
 ctgagaggag cttctgctac tctgcatcac tgatgacact cagcagggtg 2550
 atgcacagca gtctgcctcc cctatgggac tcccttctac caagcacatg 2600
 agctctctaa cagggtgggg gctaccccc gacctgctcc tacactgata 2650
 ttgaagaacc tggagaggat ccttcagttc tggccattcc agggaccctc 2700
 cagaaacaca gtgtttcaag agaccctaaa aaacctgcct gtcccaggac 2750
 cctatggtaa tgaacaccaa acatctaaac aatcatatgc taacatgcca 2800
 ctctggaaa ctccactctg aagctgccgc tttggacacc aacctccct 2850
 tctcccaggg tcatgcaggg atctgctccc tctgcttcc cttaccagtc 2900
 gtgcaccgct gactcccagg aagtctttcc tgaagtctga ccacctttct 2950
 tcttgcttca gttggggcag actctgatcc cttctgccct ggcagaatgg 3000
 caggggtaat ctgagccttc ttcactcctt taccctagct gacccttca 3050
 cctctcccc tcccttttcc tttgttttgg gattcagaaa actgcttgtc 3100
 agagactgtt tattttttat taaaaatata aggcttaaaa aaa 3143

<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met	Ala	Leu	Pro	Ala	Leu	Gly	Leu	Asp	Pro	Trp	Ser	Leu	Leu	Gly		1	5	10	15
Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr		20	25	30	
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr		35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly		50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr		65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln		80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala		95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn		110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn		125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala		140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser		155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro		170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser		185	190	195	
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg		200	205	210	
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg		215	220	225	
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr		230	235	240	
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp		245	250	255	
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys		260	265	270	
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr		275	280	285	
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro					

290										295					300				
Phe	Asn	Val	Ile	Arg	His	Ala	Val	Leu	Leu	Pro	Ala	Asp	Ser	Pro					
				305										310					315
Thr	Ala	Pro	His	Ile	Tyr	Ala	Val	Phe	Thr	Ser	Gln	Trp	Gln	Val					
				320										325					330
Gly	Gly	Thr	Arg	Ser	Ser	Ala	Val	Cys	Ala	Phe	Ser	Leu	Leu	Asp					
				335										340					345
Ile	Glu	Arg	Val	Phe	Lys	Gly	Lys	Tyr	Lys	Glu	Leu	Asn	Lys	Glu					
				350										355					360
Thr	Ser	Arg	Trp	Thr	Thr	Tyr	Arg	Gly	Pro	Glu	Thr	Asn	Pro	Arg					
				365										370					375
Pro	Gly	Ser	Cys	Ser	Val	Gly	Pro	Ser	Ser	Asp	Lys	Ala	Leu	Thr					
				380										385					390
Phe	Met	Lys	Asp	His	Phe	Leu	Met	Asp	Glu	Gln	Val	Val	Gly	Thr					
				395										400					405
Pro	Leu	Leu	Val	Lys	Ser	Gly	Val	Glu	Tyr	Thr	Arg	Leu	Ala	Val					
				410										415					420
Glu	Thr	Ala	Gln	Gly	Leu	Asp	Gly	His	Ser	His	Leu	Val	Met	Tyr					
				425										430					435
Leu	Gly	Thr	Thr	Thr	Gly	Ser	Leu	His	Lys	Ala	Val	Val	Ser	Gly					
				440										445					450
Asp	Ser	Ser	Ala	His	Leu	Val	Glu	Glu	Ile	Gln	Leu	Phe	Pro	Asp					
				455										460					465
Pro	Glu	Pro	Val	Arg	Asn	Leu	Gln	Leu	Ala	Pro	Thr	Gln	Gly	Ala					
				470										475					480
Val	Phe	Val	Gly	Phe	Ser	Gly	Gly	Val	Trp	Arg	Val	Pro	Arg	Ala					
				485										490					495
Asn	Cys	Ser	Val	Tyr	Glu	Ser	Cys	Val	Asp	Cys	Val	Leu	Ala	Arg					
				500										505					510
Asp	Pro	His	Cys	Ala	Trp	Asp	Pro	Glu	Ser	Arg	Thr	Cys	Cys	Leu					
				515										520					525
Leu	Ser	Ala	Pro	Asn	Leu	Asn	Ser	Trp	Lys	Gln	Asp	Met	Glu	Arg					
				530										535					540
Gly	Asn	Pro	Glu	Trp	Ala	Cys	Ala	Ser	Gly	Pro	Met	Ser	Arg	Ser					
				545										550					555
Leu	Arg	Pro	Gln	Ser	Arg	Pro	Gln	Ile	Ile	Lys	Glu	Val	Leu	Ala					
				560										565					570
Val	Pro	Asn	Ser	Ile	Leu	Glu	Leu	Pro	Cys	Pro	His	Leu	Ser	Ala					
				575										580					585

Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu	590	595	600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln	605	610	615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly	620	625	630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln	635	640	645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His	650	655	660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala	665	670	675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu	680	685	690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser	695	700	705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu	710	715	720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His	725	730	735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp	740	745	750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala					755	760	

<210> 278
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 278
 ctgctggtga aatctggcgt ggag 24

<210> 279
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catcttgta tgtacctggg aaccaccaca gggctcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
agggtccctt agccggggcg agggcgcgca gccagggctg agatccgcgg 50
cttccgtaga agtgagcatg gctgggcagc gaggcttct tctagtgggc 100
ttccttctcc ctggggctct gctctcagag gctgcaaaa tcttgacaat 150
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
ttcttcaaga tcacggtcac aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttaa aaaggaagaa aaatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450
ggatatcatg gattccttaa agaagagaa cttcgacatg gtgatagttg 500
aaacttttga ctactgtcct ttcctgattg ctgagaagct tgggaagcca 550
tttgtggcca ttctttccac ttcattcggc tctttggaat ttgggctacc 600
aatccccttg tcttatgttc cagtattccg ttccttgctg actgacaca 650
tggaacttctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700
aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750
tttcacagaa ggctctaggc cagttttgtc tcattctcta ctgaaagcag 800
agttgtgggt cattaactct gactttgcct ttgattttgc tcgacctctg 850
cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900

agtaccacaa gacttggaga acttcattgc caagtttggg gactctggtt 950
 ttgtccttgt gaccttgggc tccatggtga acacctgtca gaatccggaa 1000
 atcttcaagg agatgaacaa tgcctttgct cacctacccc aaggggtgat 1050
 atggaagtgt cagtgttctc attggcccaa agatgtccac ctggctgcaa 1100
 atgtgaaaat tgtggactgg ctctctcaga gtgacctcct ggctcaccca 1150
 agcatccgtc tgtttgtcac ccacggcggg cagaatagca taatggaggc 1200
 catccagcat ggtgtgcca tgggtgggat ccctctcttt ggagaccage 1250
 ctgaaaacat ggtccgagta gaagccaaaa agtttgggtgt ttctattcag 1300
 ttaaagaagc tcaaggcaga gacattggct cttaagatga aacaaatcat 1350
 ggaagacaag agatacaagt ccgcggcagt ggctgccagt gtcactctgc 1400
 gctcccaccc gctcagcccc acacagcggc tgggtgggctg gattgaccac 1450
 gtcctccaga cagggggcgc gacgcacctc aagccctatg tctttcagca 1500
 gccctggcat gagcagtacc tgttcgacgt ttttgtgttt ctgctggggc 1550
 tcactctggg gactctatgg ctttgtggga agctgctggg catggctgtc 1600
 tgggtggctgc gtggggccag aaagggtgaag gagacataag gccaggtgca 1650
 gccttggcgg ggtctgtttg gtgggcgatg tcaccatttc tagggagctt 1700
 cccactagtt ctggcagccc cattctctag tccttctagt tatctcctgt 1750
 tttcttgaag aacaggaaaa atggccaaaa atcatccttt ccacttgcta 1800
 attttgctac aaattcatcc ttactagctc ctgcctgcta gcagaaatct 1850
 ttccagtcct ctgtctctcc tttgtttgcc atcagcaagg gctatgctgt 1900
 gattctgtct ctgagtgaact tggaccactg accctcagat ttccagcctt 1950
 aaaatccacc ttccttctca tgcgcctctc cgaatcacac cctgactctt 2000
 ccagcctcca tgtccagacc tagtcagcct ctctcactcc tgcccctact 2050
 atctatcatg gaataacatc caagaaagac accttgcata ttctttcagt 2100
 ttctgttttg ttctcccaca tattctcttc aatgctcagg aagcctgccc 2150
 tgtgcttgag agttcagggc cggacacagg ctcacaggtc tccacattgg 2200
 gtccctgtct ctgggtgcca cagtgaagctc cttcttggct gagcaggcat 2250
 ggagactgta gggttccaga tttcctgaaa aataaaagt ttacagcgta 2300
 tctctcccca acctcactaa 2320

<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282
 Met Ala Gly Gln Arg Val Leu Leu Leu Val Gly Phe Leu Leu Pro
 1 5 10 15
 Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr
 20 25 30
 Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile
 35 40 45
 Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
 50 55 60
 Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
 65 70 75
 Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
 80 85 90
 Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
 95 100 105
 Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
 110 115 120
 Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
 125 130 135
 Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
 140 145 150
 Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile
 155 160 165
 Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro
 170 175 180
 Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met
 185 190 195
 Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe
 200 205 210
 Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile
 215 220 225
 Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu
 230 235 240
 Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe
 245 250 255
 Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly

260										265					270				
Leu	Met	Glu	Lys	Pro	Ile	Lys	Pro	Val	Pro	Gln	Asp	Leu	Glu	Asn					
				275					280					285					
Phe	Ile	Ala	Lys	Phe	Gly	Asp	Ser	Gly	Phe	Val	Leu	Val	Thr	Leu					
				290					295					300					
Gly	Ser	Met	Val	Asn	Thr	Cys	Gln	Asn	Pro	Glu	Ile	Phe	Lys	Glu					
				305					310					315					
Met	Asn	Asn	Ala	Phe	Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Lys					
				320					325					330					
Cys	Gln	Cys	Ser	His	Trp	Pro	Lys	Asp	Val	His	Leu	Ala	Ala	Asn					
				335					340					345					
Val	Lys	Ile	Val	Asp	Trp	Leu	Pro	Gln	Ser	Asp	Leu	Leu	Ala	His					
				350					355					360					
Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	His	Gly	Gly	Gln	Asn	Ser	Ile					
				365					370					375					
Met	Glu	Ala	Ile	Gln	His	Gly	Val	Pro	Met	Val	Gly	Ile	Pro	Leu					
				380					385					390					
Phe	Gly	Asp	Gln	Pro	Glu	Asn	Met	Val	Arg	Val	Glu	Ala	Lys	Lys					
				395					400					405					
Phe	Gly	Val	Ser	Ile	Gln	Leu	Lys	Lys	Leu	Lys	Ala	Glu	Thr	Leu					
				410					415					420					
Ala	Leu	Lys	Met	Lys	Gln	Ile	Met	Glu	Asp	Lys	Arg	Tyr	Lys	Ser					
				425					430					435					
Ala	Ala	Val	Ala	Ala	Ser	Val	Ile	Leu	Arg	Ser	His	Pro	Leu	Ser					
				440					445					450					
Pro	Thr	Gln	Arg	Leu	Val	Gly	Trp	Ile	Asp	His	Val	Leu	Gln	Thr					
				455					460					465					
Gly	Gly	Ala	Thr	His	Leu	Lys	Pro	Tyr	Val	Phe	Gln	Gln	Pro	Trp					
				470					475					480					
His	Glu	Gln	Tyr	Leu	Phe	Asp	Val	Phe	Val	Phe	Leu	Leu	Gly	Leu					
				485					490					495					
Thr	Leu	Gly	Thr	Leu	Trp	Leu	Cys	Gly	Lys	Leu	Leu	Gly	Met	Ala					
				500					505					510					
Val	Trp	Trp	Leu	Arg	Gly	Ala	Arg	Lys	Val	Lys	Glu	Thr							
				515					520										

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 283
 tgcctttgct cacctacccc aagg 24

 <210> 284
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 284
 tcaggctggt ctccaaagag aggg 24

 <210> 285
 <211> 45
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

 <400> 285
 cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

 <210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

 <400> 286
 gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50
 gggttagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100
 cccgtcacac acacatacca tgttctccat cccccaggt ccagccctca 150
 gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
 cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250
 tgctgtcact gcatgctctg ccaaggagga gggaactgca gtgacagcag 300
 gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350
 gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400
 ccagggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450

gggttgcaga gcccctcagc catgttggga gccaaagccac actggctacc 500
 aggtccccta cacagtcccg ggctgccctt ggttctggtg cttctggccc 550
 tgggggccgg gtgggccag gaggggtcag agcccgctct gctggagggg 600
 gagtgccctg tggctctgtga gcctggccga gctgctgcag gggggcccgg 650
 gggagcagcc ctgggagagg caccctctgg gcgagtggca tttgctgcgg 700
 tccgaagcca ccaccatgag ccagcagggg aaaccggcaa tggcaccagt 750
 ggggccatct acttcgacca ggtcctggtg aacgagggcg gtggctttga 800
 ccgggcctct ggctccttcg tagccctgt ccggggtgtc tacagcttcc 850
 ggttccatgt ggtgaaggtg tacaaccgcc aaactgtcca ggtgagcctg 900
 atgctgaaca cgtggcctgt catctcagcc tttgccaatg atcctgacgt 950
 gaccggggag gcagccacca gctctgtgct actgcccttg gaccctgggg 1000
 accgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050
 tactcaagtt tctctggctt cctcatcttc cctctctgag gacccaagtc 1100
 tttcaagcac aagaatccag cccctgacaa ctttcttctg ccctctcttg 1150
 cccagaaac agcagaggca ggagagagac tccctctggc tcctatccca 1200
 cctctttgca tgggacctg tgccaaacac ccaagtttaa gagaagagta 1250
 gagctgtggc atctccagac caggcctttc caccaccca ccccagtta 1300
 ccctcccagc cacctgctgc atctgttctt gcctgcagcc ctaggatcag 1350
 ggcaagggtt ggcaagaagg aagatctgca ctactttgcg gcctctgctc 1400
 ctccggttcc cccaccccag ctctctgctc aatgctgac agggacaggt 1450
 ggcgcaggtg agcctgacag gccccacag gagcccagat ggacaagcct 1500
 cagcgtaccc tgcaggcttc ttctgtgag gaaagccagc atcacggatc 1550
 tcagccagca ccgtcagaag ctgagccagc accgtatggg ctagggtggg 1600
 aggtcagcc acaggcagaa ggggtgggaag ggcctggagt ctgtggctgg 1650
 tgaggaagga aggaggggtg attgtctaga ctgaacatgg tacacattct 1700
 gcatgtatag cagagcagcc agcaggtagc aatcctggct gtccttctat 1750
 gctggatccc agatggactc tggcccttac ctccccacct gagattaggg 1800
 tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850
 ctggaagtgg accatggaaa acatcgataa ccatgcatcc tcttgcttgg 1900

ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950
 cactctgact gctgcctcct tcctcccagc tctctcactg agttatcttc 2000
 actgtacctg ttccagcata tccccactat ctctctttct cctgatctgt 2050
 gctgtcttat tctcctcctt aggccttccta ttacctggga ttccatgatt 2100
 cattccttca gaccctctcc tgccagtatg ctaaaccctc cctctctctt 2150
 tcttatcccg ctgtccatt ggcccagcct ggatgaatct atcaataaaa 2200
 caactagaga atggtggtca gtgagacact atagaattac taaggagaag 2250
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatgttgc 2300
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
1				5					10					15
Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

	170		175		180
Leu Arg Leu Arg	Arg Gly Asn Leu Leu	Gly Gly Trp Lys Tyr	Ser		
	185	190	195		
Ser Phe Ser Gly	Phe Leu Ile Phe Pro Leu				
	200	205			

<210> 288
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 288
 aggcagccac cagctctgtg ctac 24

<210> 289
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 289
 cagagaggga agatgaggaa gccagag 27

<210> 290
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-42
 <223> Synthetic construct.

<400> 290
 ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 291
 gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50
 tagccgcca gcctcgacgc cgtcccgga cccctgtgct ctgcgcgaag 100
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200
 ccgcctactc cggggtcctg cgcggcgagc gtcaggccga ggctgaccgg 250
 agccagcgct ctacagggag acctgcgctg tcgcgcgagg ggtctgggag 300
 atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350
 tcacctggct caatagggtcc aagggtgaaa agcagctaca ggtcatctca 400
 gtgctccagt gggctctgtc cttccttgta ctgggagtgg cctgcagtgc 450
 catectcatg tacatatctt gacttgattg ctggctcacc gctgtgctct 500
 acttcacttg gctgggtgtt gactggaaca cacccaagaa aggtggcagg 550
 aggtcacagt ggggccgaaa ctgggctgtg tggcgctact ttcgagacta 600
 ctttcccatc cagctgggtga agacacacaa cctgctgacc accaggaact 650
 atatcttttg ataccacccc catggtatca tgggcctggg tgccttctgc 700
 aacttcagca cagaggccac agaagtgagc aagaagttcc caggcatacg 750
 gccttacctg gctacactgg caggcaactt ccgaatgcct gtgttgaggg 800
 agtacctgat gtctggaggt atctgccctg tcagccggga caccatagac 850
 tatttgcttt caaagaatgg gagtggcaat gctatcatca tcgtggctcg 900
 ggggtgcggct gagtctctga gctccatgcc tggcaagaat gcagtcaccc 950
 tgcggaaccg caagggtctt gtgaaactgg ccctgcgtca tggagctgac 1000
 ctgggttccca tctactcctt tggagagaat gaagtgtaca agcaggtgat 1050
 cttcgaggag ggctcctggg gccgatgggt ccagaagaag ttccagaaat 1100
 acattggttt cgcccatgc atcttccatg gtcgaggcct cttctcctcc 1150
 gacacctggg ggctggtgcc ctactccaag cccatcacca ctgttggtgg 1200
 agagcccatc accatcccca agctggagca cccaaccag caagacatcg 1250
 acctgtacca caccatgtac atggaggccc tgggtaagct cttcgacaag 1300
 cacaagacca agttcggcct cccggagact gaggtcctgg aggtgaactg 1350
 agccagcctt cggggccaat tccctggagg aaccagctgc aaatcacttt 1400
 tttgctctgt aaatttgtaa gtgtcatggg tgtctgtggg ttatttaaaa 1450
 gaaattataa caattttgct aaacaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550
 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu	1	5	10	15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro	20	25	30	
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	35	40	45	
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	50	55	60	
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	65	70	75	
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	80	85	90	
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	95	100	105	
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	110	115	120	
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	125	130	135	
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	140	145	150	
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	155	160	165	
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	170	175	180	
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu	185	190	195	
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser	200	205	210	
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu	215	220	225	
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly	230	235	240	
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	245	250	255	
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly				

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr	280	285
275		
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln	295	300
290		
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His	310	315
305		
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr	325	330
320		
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro	340	345
335		
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr	355	360
350		
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr	370	375
365		
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn	385	
380		

<210> 293

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 293

gctgacctgg ttcccatcta ctcc 24

<210> 294

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
gggcggcggg atggggggccg ggggcggcgg gcgccgcact cgctgaggcc 50
ccgacgcagg gccggggccg gcccagggcc gaggagcgcg gcggccagag 100
cggggccgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
ggctctgctg accttgtgcc ttggacggct gtcctcagcg aggggccgtg 250
caccgctcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300
gttcgtgctg cacctgctgg tcggctttgt cttcgtggtg agtggctctg 350
tcatcaactt cgtccagctg tgcacgctgg cgtcttgcc ggtcagcaag 400
cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450
actggtcatg ctgctggagt ggtggtcctg cacggagtgt aactgttca 500
cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550
ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600
gcgcttcgga gtgctgggga gtcceaagg cctcgctaag aaggagctgc 650
tctacgtgcc cctcatcgcc tggacgtggt actttctgga gattgtgttc 700
tgcaagcggg agtgggagga ggaccgggac accgtgggtc aagggtgag 750
gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgcgagg 800
ggacgcgctt cacggagacc aagcacgcg ttagcatgga ggtggcggct 850
gctaaggggc ttctgtcct caagtaccac ctgctgccgc ggaccaaggg 900
cttcaccacc gcagtcaagt gcctccgggg gacagtcgca gctgtctatg 950
atgtaaccct gaacttcaga ggaaacaaga acccgtcctt gctggggatc 1000
ctctacggga agaagtacga ggcgacatg tgcgtgagga gatttcctct 1050
ggaagacatc ccgctggatg aaaaggaagc agctcagtgg cttcataaac 1100
tgtaccagga gaaggacgcg ctccaggaga tatataatca gaaggcatg 1150

ttccagggg agcagtttaa gcctgcccg aggccgtgga cctcctgaa 1200
 ctctctgtcc tgggccacca ttctcctgtc tcccctcttc agttttgtct 1250
 tgggcgtctt tgccagcgga tcacctctcc tgatcctgac tttcttgggg 1300
 tttgtgggag cagcttcctt tggagttcgc agactgatag gagaatcgct 1350
 tgaacctggg aggtggagat tgcagtgagc tgagatggca tctactgtact 1400
 ccagcctagg caacagagca agactcagtc tcaaaaaaaaa aaaaaaaca 1450
 aaaaacccca gaaattctgg agttgaactg tgtagttact gacatgaaaa 1500
 attcactaga ggctgaacag cagatttgag caggcagaaa aaaatcagca 1550
 agcttgaaga tggtagcttg agatttttca ggctaataaa aaaagaatga 1600
 agggaaatta acagcctcag agacccatgg tgcaccgtca cacaatcaa 1650
 catatgcatg atgagagtcc cagaaggaga ggagagaaag ggtcagaaag 1700
 aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750
 gtgaactcca atgaggatga atatcagaga tccacaccta gatatttcat 1800
 aatcaaagtg tcaaatgaca aagaatcttg aaagcagcaa gagatgagca 1850
 acttatcttg ttcaaaggat ctttgatcag attaacagct catttctcct 1900
 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000
 ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050
 aagcttcctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100
 ttacacctgt aatcccagca ctttgggagg ccagacggg tggatcattt 2150
 ggggtcaggc tgatctcaaa ctctgagtt caggtgatct gcccgacctca 2200
 gcctccaaa gtgttgatg tgcaggcgtg agccactgcg cctggccgga 2250
 atttcttttt aaggctgaat gatgggggccc aggcacgatg gtcacgcct 2300
 gtgatcccaa gtagcttgga ttgtaaacat gcaccacat gcctggctaa 2350
 tttttgtatt ttagtagag acgtgttagc caggctggtc tcgatctcct 2400
 gacctcaagt gaccacctgc ctacagcctcc caaagtactg ggattacagg 2450
 cgtgagccac tgtgcctggc cttgagcatc ttgtgatgtg cttattggcc 2500
 atttgatat cttctatctt ctttggggaa atgtctgttc aagtcctttg 2550
 cctttttaaa tttttattat ttatttattt atttattttg agacagggtc 2600

ttgttctgtt gccaggctg gactacagt gcacagtctt ggctcactgc 2650
 agcctcgacc tcctgggctg cagtgatect cccacctcag cctcccttgt 2700
 agctgtatatt tttgtatatt tgtattttgt agctgtagtt tttgtatatt 2750
 ttgtggagac agcatttcac catgatgccc aggtcgggtct tgaactcctg 2800
 agctcaagtg atctgcctgc ttcagcctcc caaagtgctg ggattacaga 2850
 catgagccac tgcacctggc aaactcccaa aattcaacac acacacacaa 2900
 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gccccaacta 2950
 ccaggagagac tgaagtggga ggatcgcttg ggcatgagaa gtcgaggctg 3000
 cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagtgag 3050
 accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu	1	5	10	15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	20	25	30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	35	40	45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	65	70	75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala	80	85	90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr	125	130	135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu	140	145	150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr	155	160	165	

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	170	175	180
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	185	190	195
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	200	205	210
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	215	220	225
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	230	235	240
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	245	250	255
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	260	265	270
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	275	280	285
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	290	295	300
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	305	310	315
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	320	325	330
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	335	340	345
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	350	355	360
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								365		

<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttcctctgt gggtagacca tgtg 24

<210> 299

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgcccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

gatattcttt attttaaga atctgaagta ctatgcatca ctccctccaa 50
tgtcctgggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100
tgcttttagca ctggggcact tcttgcttat ttctttggta ggaaaggggc 150
tcagtttgtc ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200
cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250
tagctgggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300
ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350
ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400
gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450
tgtcggtcct gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500
tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550
atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600
ctggcctgac agaattctcat cttgtttaat gctctcataa gaccacttgt 650
ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700
gttgtagtgg ttgtgtctgt tccccagaat gccagctct gagctgcgtg 750

aggggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctca gttcaccaga tgggtgtaggg cccagcattg taaattcaca 900
 cgttgactgt gcttgtgaat tatctgggga tgcaggtcct gattcagtag 950
 gccagggttg ggcattctcta acaaactccc acgtgatgct gatgctggtc 1000
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050
 tggctcacac ctatgatccc agcactttgg gaggctgagg caggctgata 1100
 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150
 tctgtactaa aaatacacaa attagctggg catggtggca catgcctgta 1200
 gtcccagcta cttgggaggg tgaagcaaga gaatcgcttg aacctgggag 1250
 gcggagggtg cagtgaagcc agatcaggcc actgtattcc aaccagggtg 1300
 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile	1	5	10	15
His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe	20	25	30	
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly	35	40	45	
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val	50	55	60	
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp	65	70	75	
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr	80	85	90	
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln	95	100	105	
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu	110	115	120	
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr	125	130	135	
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu											

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
 ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc 50
 aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100
 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
 tatgtctgtg tggtagtgc tctactcct acctacatta aaatctgttt 200
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300
 ttctaccac accgtcccct cgaagccggg gacagcctca ccttgcctggc 350
 ctctcgctgg agcagtggcc tcaccaactg tctcacgtct ggaggcactg 400
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450
 tgggccttgc cctggccgta gaagggattg acaagcccga agatttcata 500
 ggcgatggct cccactggcc aggcatcagc cttgctgtag tcaatcactg 550
 ccctggggcc aggacgggcc gtggacacct gctcagaagc agtgggtgag 600
 acatcacgct gcccgcccat ctaacctttt catgtcctgc acatcacctg 650
 atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga 700
 gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750
 acaggacttg cattctcctg gaacatgagg gaacgccgga ggaaagcaaa 800
 gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850
 gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900
 ggaagggtcg ccgatggcg atgacacact cgggactcac ctctggggcc 950
 atcagacagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa 1000
 ctgcaggccg atgctctcat cagccaggca gcagccaaaa tctgcgatca 1050
 ccagccaggg gcagccgtct gggaaggagc aagcaaagtg accatttctc 1100
 ctcccctcct tccctctgag aggccctcct atgtccctac taaagccacc 1150
 agcaagacat agctgacagg ggctaattgg tcagtgttgg ccaggaggt 1200
 cagcaaggcc tgagagctga tcagaaggcc ctgctgtgcg aacacggaaa 1250

tgctccagt aagcacaggc tgcaaatcc ccaggcaaag gactgtgtgg 1300
 ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaagg 1350
 agctagagct tggttcaaat gatctccaag ggcccttata cccagggaga 1400
 ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccaggtgcat 1450
 taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacattttgg 1500
 gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550
 gccaacatgg tgaaaccctt gtctctacta aaaatacaaa aaaactagcc 1600
 aggcattgtg gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
 ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag 1750
 aattatgggt atttgtaa 1768

<210> 304
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 304
 Met Leu Trp Trp Leu Val Leu Leu Leu Leu Pro Thr Leu Lys Ser
 1 5 10 15
 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
 20 25 30
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
 65 70 75
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
 80 85 90
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
 95 100 105
 Arg Arg Arg Asp

<210> 305
 <211> 989
 <212> DNA
 <213> Homo sapiens

<400> 305

gcggggccgc gagtccgaga cctgtcccag gagctccagc tcacgtgacc 50
 tgtcactgcc tcccgcgcgc tcctgcccgc gccatgaccc agccggtgcc 100
 ccggtctctc gtgcccgcgc cgctggccct gggctcagcc gcaactgggcg 150
 ccgccttcgc cactggcctc ttcctgggga ggcggtgccc cccatggcga 200
 ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250
 gtatcttctg agccgctcca tgcgggagca cccggcgctg cgaagcctga 300
 ggctgctgac cctggagcag ccgcaggggg attctatgat gacctgcgag 350
 caggcccagc tcttggccaa cctggcgcgg ctcatccagg ccaagaaggc 400
 gctggacctg ggcaccttca cgggctactc cgccctggcc ctggccctgg 450
 cgctgcccgc ggacggggcg gtggtgacct gcgaggtgga cgcgcagccc 500
 ccggagctgg gacggcccct gtggaggcag gccgaggcgg agcacaagat 550
 cgacctccgg ctgaagcccg ccttggagac cctggacgag ctgctggcgg 600
 cgggcgaggc cggcaccttc gacgtggccg tgggtgatgc ggacaaggag 650
 aactgctccg cctactacga gcgctgcctg cagctgctgc gacccggagg 700
 catectcgcc gtcctcagag tcctgtggcg cgggaagggtg ctgcaacctc 750
 cgaaagggga cgtggcggcc gagtgtgtgc gaaacctaaa cgaacgcatac 800
 cggcgggacg tcagggtcta catcagcctc ctgcccctgg gcgatggact 850
 caccttggcc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900
 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala
1				5					10					15

Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
			20						25					30

Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45

Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55					60

Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	65	70	75
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	80	85	90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	95	100	105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	110	115	120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	125	130	135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	140	145	150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	155	160	165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	170	175	180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	185	190	195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	200	205	210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	215	220	225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	230	235	240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	245	250	255
Leu	Thr	Leu	Ala	Phe	Lys	Ile									260		

<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

```

ccgccgccgc agccgctacc gccgctgcag ccgctttccg cggcctgggc 50
ctctcgccgt cagcatgccca cacgccttca agcccgggga cttggtgttc 100
gctaagatga agggctaccc tcaactggcct gccaggatcg acgacatcgc 150
ggatggcgcc gtgaagcccc cacccaacaa gtaccccatc tttttctttg 200
gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

```

aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300
 agggctgtgg gagatccaga acaacccccca cgccagctac agcgcccctc 350
 cgccagttag ctcctccgac agcgaggccc ccgaggccaa ccccgccgac 400
 ggcagttagc ctgacgagga cgatgaggac cggggggtca tggccgtcac 450
 agcggttaacc gccacagctg ccagcgacag gatggagagc gactcagact 500
 cagacaagag tagcgacaac agtggcctga agaggaagac gcctgcgcta 550
 aagatgtcgg tctcgaaacg agcccgaag gcctccagcg acctggatca 600
 ggccagcgtg tccccatccg aagaggagaa ctcggaaagc tcctctgagt 650
 cggagaagac cagcgaccag gacttcacac ctgagaagaa agcagcggtc 700
 cgggcgccac ggagggggccc tctgggggga cggaaaaaaa agaaggcgcc 750
 gtcagcctcc gactccgact ccaaggccga ttcggacggg gccaaagcctg 800
 agccggtggc catggcgcgg tcggcgctct cctcctctc ttcctcctcc 850
 tcctccgact ccgatgtgtc tgtgaagaag cctccgaggg gcaggaagcc 900
 agcggagaag cctctcccga agccgcgagg gcggaaaccg aagcctgaac 950
 ggctccgctc cagctccagc agtgacagtg acagcgacga ggtggaccgc 1000
 atcagttagt ggaagcggcg ggacgaggcg cggaggcgcg agctggaggc 1050
 ccggcgcgcg cgagagcagg aggaggagct gcggcgccctg cgggagcagg 1100
 agaaggagga gaaggagcgg aggcgcgagc gggccgaccg cggggaggct 1150
 gagcggggca gcggcggcag cagcggggac gagctcaggg aggacgatga 1200
 gcccgctcaag aagcggggac gcaagggccg gggccggggt ccccgctcct 1250
 cctctgactc cgagcccag gccgagctgg agagagaggc caagaaatca 1300
 gcgaagaagc cgcagtcctc aagcacagag cccgccagga aacctggcca 1350
 gaaggagaag agagtgcggc ccgaggagaa gcaacaagcc aagcccgtga 1400
 aggtggagcg gacccggaag cggtcgagg gcttctcgat ggacaggaag 1450
 gtagagaaga agaaagagcc ctccgtggag gagaagctgc agaagctgca 1500
 cagttagatc aagtttgccc taaaggctga cagcccggac gtgaagaggt 1550
 gcctgaatgc cctagaggag ctgggaaccc tgcaggtgac ctctcagatc 1600
 ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttcgccgtta 1650
 caaagcgaac aaggacgtaa tggagaaggc agcagaagtc tatacccggc 1700

tcaagtcgcg ggtcctcggc ccaaagatcg aggcggtgca gaaagtgaac 1750
aaggctggga tggagaagga gaaggccgag gagaagctgg ccggggagga 1800
gctggccggg gaggaggccc cccaggagaa ggcggaggac aagcccagca 1850
ccgatctctc agccccagtg aatggcgagg ccacatcaca gaagggggag 1900
agcgcagagg acaaggagca cgaggagggt cgggactcgg aggaggggcc 1950
aagggtgtggc tcctctgaag acctgcacga cagcgtacgg gaggggtccc 2000
acctggacag gcctgggagc gaccggcagg agcgcgagag ggcacggggg 2050
gactcggagg ccctggacga ggagagctga gccgcgggca gccaggccca 2100
gccccgccc gagctcaggc tgcccctctc cttccccggc tcgcaggaga 2150
gcagagcaga gaactgtggg gaacgctgtg ctgtttgtat ttgttcctt 2200
gggttttttt ttcctgccta atttctgtga tttccaacca acatgaaatg 2250
actataaacg gttttttaat ga 2272

<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met	1	5	10	15
Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp	20	25	30	
Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe	35	40	45	
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro	50	55	60	
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys	65	70	75	
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala	80	85	90	
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala	95	100	105	
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp	110	115	120	
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala	125	130	135	
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser				

140										145					150				
Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser					
				155					160					165					
Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala					
				170					175					180					
Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu					
				185					190					195					
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala					
				200					205					210					
Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys					
				215					220					225					
Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser					
				230					235					240					
Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser					
				245					250					255					
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Asp	Val	Ser	Val					
				260					265					270					
Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro					
				275					280					285					
Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser					
				290					295					300					
Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu					
				305					310					315					
Trp	Lys	Arg	Arg	Asp	Glu	Ala	Arg	Arg	Arg	Glu	Leu	Glu	Ala	Arg					
				320					325					330					
Arg	Arg	Arg	Glu	Gln	Glu	Glu	Glu	Leu	Arg	Arg	Leu	Arg	Glu	Gln					
				335					340					345					
Glu	Lys	Glu	Glu	Lys	Glu	Arg	Arg	Arg	Glu	Arg	Ala	Asp	Arg	Gly					
				350					355					360					
Glu	Ala	Glu	Arg	Gly	Ser	Gly	Gly	Ser	Ser	Gly	Asp	Glu	Leu	Arg					
				365					370					375					
Glu	Asp	Asp	Glu	Pro	Val	Lys	Lys	Arg	Gly	Arg	Lys	Gly	Arg	Gly					
				380					385					390					
Arg	Gly	Pro	Pro	Ser	Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu					
				395					400					405					
Glu	Arg	Glu	Ala	Lys	Lys	Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser					
				410					415					420					
Thr	Glu	Pro	Ala	Arg	Lys	Pro	Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg					
				425					430					435					

Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr	
				440					445					450	
Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys	
				455					460					465	
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser	
				470					475					480	
Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	
				485					490					495	
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	
				500					505					510	
Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys	
				515					520					525	
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala	
				530					535					540	
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile	
				545					550					555	
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	
				560					565					570	
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	
				575					580					585	
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	
				590					595					600	
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	
				605					610					615	
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	
				620					625					630	
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	
				635					640					645	
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	
				650					655					660	
Arg	Gly	Asp	Ser	Glu	Ala	Leu	Asp	Glu	Glu	Ser					
				665					670						

<210> 309

<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

gttggttctc ctggatcttc accttaccaa ctgcagatct tgggactcat 50

cagcctcaat aattatatta aattaacacc atttgaaaga gaacattggt 100

ttcatcatga atgctaataa agatgaaaga cttaaagcca gaagccaaga 150
 ttttcacctt tttcctgctt tgatgatgct aagcatgacc atgttgtttc 200
 ttccagtcac tggcactttg aagcaaaata ttccaagact caagctaacc 250
 tacaagact tgctgctttc aaatagctgt attccctttt tgggttcac 300
 agaaggactg gattttcaaa ctcttctctt agatgaggaa agaggcaggc 350
 tgctcttggg agccaaagac cacatctttc tactcagtct ggttgactta 400
 aacaaaaatt ttaagaagat ttattggcct gctgcaaagg aacgggtgga 450
 attatgtaaa ttagctggga aagatgcaa tacagaatgt gcaaatttca 500
 tcagagtact tcagccctat aacaaaactc acatatatgt gtgtggaact 550
 ggagcatttc atccaatatg tgggtatatt gatcttgag tctacaagga 600
 ggatattata ttcaactag acacacataa tttggagtct ggcagactga 650
 aatgtccttt cgatcctcag cagccttttg cttcagtaat gacagatgag 700
 tacctetact ctggaacagc ttctgatttc cttggcaaag atactgcatt 750
 cactcgatcc cttgggccta ctcatgacca ccactacatc agaactgaca 800
 tttcagagca ctactggctc aatggagcaa aatttattgg aactttcttc 850
 ataccagaca cctacaatcc agatgatgat aaaatatatt tcttctttcg 900
 tgaatcatct caagaaggca gtacctcga taaaaccatc ctttctcgag 950
 ttggaagagt ttgtaagaat gatgtaggag gacaacgcag cctgataaac 1000
 aagtggacga cttttcttaa ggccagactg atttgctcaa ttcttggaag 1050
 tgatggggca gatacttact ttgatgagct tcaagatatt tatttactcc 1100
 ccacaagaga tgaaagaaat cctgtagtat atggagtctt tactacaacc 1150
 agctccatct tcaaaggctc tgctgtttgt gtgtatagca tggctgacat 1200
 cagagcagtt tttaatggc catatgctca taaggaaagt gcagaccatc 1250
 gttgggtgca gtatgatggg agaattcctt atccacggcc tggatcatgt 1300
 ccaagcaaaa cctatgacc actgattaag tccacccgag attttccaga 1350
 tgatgtcatc agtttcataa agcggcactc tgtgatgtat aagtccgtat 1400
 acccagttgc aggaggacca acgttcaaga gaatcaatgt ggattacaga 1450
 ctgacacaga tagtgggtgga tcatgtcatt gcagaagatg gccagtacga 1500
 tgtaatgttt cttggaacag acattggaac tgtcctcaaa gttgtcagca 1550

tttcaaagga aaagtggaat atggaagagg tagtgctgga ggagttgcag 1600
 atattcaagc actcatcaat catcttgaac atggaattgt ctctgaagca 1650
 gcaacaattg tacattggtt cccgagatgg attagttcag ctctccttgc 1700
 acagatgcga cacttatggg aaagcttgcg cagactgttg tcttgccaga 1750
 gacccctact gtgcctggga tggaaatgca tgctctcgat atgctcctac 1800
 ttctaaaagg agagctagac gccaaagatgt aaaatatggc gacccaatca 1850
 cccagtgtg ggacatcgaa gacagcatta gtcatgaaac tgctgatgaa 1900
 aaggtgattt ttggcattga atttaactca acctttctgg aatgtatacc 1950
 taaatcccaa caagcaacta ttaaattgta tatccagagg tcaggggatg 2000
 agcatcgaga ggagttgaag cccgatgaaa gaatcatcaa aacggaatat 2050
 gggctactga ttcgaagttt gcagaagaag gattctggga tgtattactg 2100
 caaagcccag gagcacactt tcatccacac catagtgaag ctgactttga 2150
 atgtcattga gaatgaacag atggaaaata cccagagggc agagcatgag 2200
 gaggggcagg tcaaggatct attggctgag tcacggttga gatacaaaga 2250
 ctacatccaa atccttagca gcccaaactt cagcctcgac cagtactgcg 2300
 aacagatgtg gcacagggag aagcggagac agagaaacaa ggggggcca 2350
 aagtggaagc acatgcagga aatgaagaag aaacgaaatc gaagacatca 2400
 cagagacctg gatgagctcc ctagagctgt agccacgtag ttttctactt 2450
 aatttaaaga aaagaattcc ttacctataa aaacattgcc ttctgttttg 2500
 tataatccctt atagtaattc ataaatgctt cccatggagt ttgctaagg 2550
 cacaagacaa taatctgaat aagacaatat gtgatgaata taagaaagg 2600
 caaaaaattc atttgaacca gttttccaag aacaaatctt gcacaagcaa 2650
 agtataagaa ttatcctaaa aatagggggt ttacagttgt aaatgtttta 2700
 tgttttgagt ttggaattt attgtcatgt aaatagttga gctaagcaag 2750
 cccgaattt gatagtgtat aaggtgcttt attccctcga atgtccatta 2800
 agcatggaat ttaccatgca gttgtgctat gttcttatga acagatatat 2850
 cattcctatt gagaaccagc taccttgtgg tagggaataa gaggtcagac 2900
 acaaattaag acaactccca ttatcaacag gaactttctc agtgagccat 2950
 tcactcctgg agaattgtat aggaatttgg agaggtgcat tatttctttc 3000

tggccactgg gggttaaattt agtgtactac aacattgatt tactgaaggg 3050
 cactaatgtt tccccagga tttctattga ctagtcagga gtaacagggt 3100
 cacagagaga agttggtgct tagttatgtg ttttttagag tatatactaa 3150
 gctctacagg gacagaatgc ttaataaata cttaataag atatgggaaa 3200
 atattttaat aaaacaagga aaacataatg atgtataatg catcctgatg 3250
 ggaaggcatg cagatgggat ttgttagaag acagaaggaa agacagccat 3300
 aaattctggc tttggggaaa actcatatcc ccatgaaaag gaagaacaat 3350
 cacaaataaa gtgagagtaa tgtaatggag ctcttttcac tagggataa 3400
 gtagctgcca atttgtaatt catctgttaa aaaaaatcta gattataaca 3450
 aactgctagc aaaatctgag gaaacataaa ttcttctgaa gaatcatagg 3500
 aagagtagac attttattta taaccaatga tatttcagta tatattttct 3550
 ctcttttaaa aaatatttat catactctgt atattatttc tttttactgc 3600
 ctittattct tctgtatat tggattttgt gattatattt gagtgaatag 3650
 gagaaaacaa tatataacac acagagaatt aagaaaatga catttctggg 3700
 gagtggggat atatatttgt tgaataacag aacgagtgt aaattttaac 3750
 aacggaaagg gttaaattaa ctctttgaca tcttactca accttttctc 3800
 attgctgagt taatctgttg taattgtagt attgtttttg taatttaaca 3850
 ataaataagc ctgctacatg t 3871

<210> 310
 <211> 777
 <212> PRT
 <213> Homo sapiens

<400> 310
 Met Asn Ala Asn Lys Asp Glu Arg Leu Lys Ala Arg Ser Gln Asp
 1 5 10 15
 Phe His Leu Phe Pro Ala Leu Met Met Leu Ser Met Thr Met Leu
 20 25 30
 Phe Leu Pro Val Thr Gly Thr Leu Lys Gln Asn Ile Pro Arg Leu
 35 40 45
 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
 50 55 60
 Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
 65 70 75
 Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

80										85					90				
Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile					
				95					100					105					
Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala					
				110					115					120					
Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu					
				125					130					135					
Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala					
				140					145					150					
Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu					
				155					160					165					
Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg					
				170					175					180					
Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met					
				185					190					195					
Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly					
				200					205					210					
Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His					
				215					220					225					
His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly					
				230					235					240					
Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro					
				245					250					255					
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu					
				260					265					270					
Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val					
				275					280					285					
Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp					
				290					295					300					
Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser					
				305					310					315					
Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu					
				320					325					330					
Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe					
				335					340					345					
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr					
				350					355					360					
Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His					
				365					370					375					

Lys Glu Ser Ala Asp His Arg Trp Val Gln Tyr Asp Gly Arg Ile	380	385	390
Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys Thr Tyr Asp Pro	395	400	405
Leu Ile Lys Ser Thr Arg Asp Phe Pro Asp Asp Val Ile Ser Phe	410	415	420
Ile Lys Arg His Ser Val Met Tyr Lys Ser Val Tyr Pro Val Ala	425	430	435
Gly Gly Pro Thr Phe Lys Arg Ile Asn Val Asp Tyr Arg Leu Thr	440	445	450
Gln Ile Val Val Asp His Val Ile Ala Glu Asp Gly Gln Tyr Asp	455	460	465
Val Met Phe Leu Gly Thr Asp Ile Gly Thr Val Leu Lys Val Val	470	475	480
Ser Ile Ser Lys Glu Lys Trp Asn Met Glu Glu Val Val Leu Glu	485	490	495
Glu Leu Gln Ile Phe Lys His Ser Ser Ile Ile Leu Asn Met Glu	500	505	510
Leu Ser Leu Lys Gln Gln Gln Leu Tyr Ile Gly Ser Arg Asp Gly	515	520	525
Leu Val Gln Leu Ser Leu His Arg Cys Asp Thr Tyr Gly Lys Ala	530	535	540
Cys Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp	545	550	555
Gly Asn Ala Cys Ser Arg Tyr Ala Pro Thr Ser Lys Arg Arg Ala	560	565	570
Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp	575	580	585
Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val	590	595	600
Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro	605	610	615
Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly	620	625	630
Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys	635	640	645
Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser	650	655	660
Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr			

665	670	675
Ile Val Lys Leu Thr Leu Asn Val Ile	Glu Asn Glu Gln Met Glu	
680	685	690
Asn Thr Gln Arg Ala Glu His Glu Glu	Gly Gln Val Lys Asp Leu	
695	700	705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys	Asp Tyr Ile Gln Ile Leu	
710	715	720
Ser Ser Pro Asn Phe Ser Leu Asp Gln	Tyr Cys Glu Gln Met Trp	
725	730	735
His Arg Glu Lys Arg Arg Gln Arg Asn	Lys Gly Gly Pro Lys Trp	
740	745	750
Lys His Met Gln Glu Met Lys Lys Lys	Arg Asn Arg Arg His His	
755	760	765
Arg Asp Leu Asp Glu Leu Pro Arg Ala	Val Ala Thr	
770	775	

<210> 311
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 311
 caacgcagcc gtgataaaca agtgg 25

<210> 312
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 312
 gcttgacat gtaccaggcc gtgg 24

<210> 313
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 313
ggccagactg atttgctcaa ttcctggaag tgatggggca gatac 45

<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

<400> 314
ccctgacctc cctgagccac actgagctgg aagccgcaga ggtcatcctg 50
gagcatgccc accgcgggga gcagacaacc tcccaggtaa gctgggagca 100
agacctgaag ctgtttcttc aggagcctgg tgtattttcc cccacccac 150
ctcagcagtt tcagccagca gggactgatc aggtgtgtgt cctggagtgg 200
ggagcagaag gcgtggctgg caagagtggc ctggagaaag aggttcagcg 250
cttgaccagc cgagctgccc gtgactacaa gatccagaac catgggcatc 300
gggtgaggtg ggggggcaca ggtgtcatgt gcaccttctt gtctcagcaa 350
gaagagctga gagaggggat cttggagcca ttgaggggtg catggagcta 400
cagaggggag ggaaaggtat ttaaggtaa cagtgtggca caatagttaa 450
gagcacagtt tttggagcta gaccgacata ggttcaaatt ctcttctgtt 500
gcttcctagt tctgtagccc caggtaaggg agtgacttaa cctctctgga 550
cttcaatttc ctcatcacta aagtagggcc aataatagca cccacctcat 600
agggaagatt aaatgacata atgtatgtga tgcaactagc aaagtaccag 650
tcccatagta agtcatgccc cacagtattt ccacccaccc ctgttctctg 700
ccttcccaac caggtaactgc aacgactgga gcagaggcgg cagcaggctt 750
cagagcggga ggctccaagc atagaacaga ggttacagga agtgcgagag 800
agcatccgcc gggcacaggt gagccaggtg aagggggctg cccggctggc 850
cctgctgcag ggggctggct tagatgtgga gcgctggctg aagccagcca 900
tgaccagcgc ccaggatgag gtggagcagg agcggcggct cagtgaggct 950
cggctgtccc agagggacct ctctccaacc gctgaggatg ctgagctttc 1000
tgactttgag gaatgtgagg agacgggaga gctctttgag gagcctgccc 1050
cccaagccct ggccacgagg gccctccct gccctgcaca cgtgggtattt 1100
cgctatcagg cagggcggtga ggatgagctg acaatcacgg agggtgagtg 1150
gctggaggtc atagaggagg gagatgctga cgaatgggtc aaggctcgga 1200
accagcacgg cgaggtaggc tttgtccctg agcgatatct caacttcccg 1250

gacctctccc tcccagagag cagccaagac agtgacaatc cctgcggggc 1300
agagcccaca gcattcctgg cacaggccct gtacagctac accggacaga 1350
gtgcagagga gctgagcttc cctgaggggg cactcatccg tctgctgccc 1400
cgggcccag atggagtaga tgacggcttc tggaggggag aatttggggg 1450
ccgtgttggg gtcttcccct ccctgctggt ggaagagctg cttggcccc 1500
cagggccacc tgaactctct gaccctgaac agatgctgcc gtccccctt 1550
cctcccagct tctccccacc tgcacctacc tctgtgttg atgggcccc 1600
tgcacctgtc ctgcctgggg acaaagccct ggacttcctt gggttcctgg 1650
acatgatggc acctcgactc aggccgatgc gtccaccacc tccccgccg 1700
gctaaagccc cggatcctgg ccaccagat cccctcacct gaaggccagg 1750
gaagccttga cccccagtga tgctgctgtc cctatcttca agctgtcaga 1800
ccacaccatc aatgatccag agcaacacag ccaaagctg gaatcgccct 1850
tatttccacc ctacacctca aggggtgaaa cttgcccctt cccatttcta 1900
gagctggaac ccactccttt ttttccatt gttctatcat ctctaggacc 1950
ggaactacta ccttctcttc tgtcatgacc ctatctaggg tggtgaaatg 2000
cctgaaatct ctggggctgg aaaccatcca tcaaggtctc tagtagttct 2050
ggccacctc tttccccacc ctggctccat gaccacccc actctggatg 2100
ccagggtcac tggggttggg ctggggagag gaacaggcct tgggaatcag 2150
gagctggagc caggatgcga agcagctgta atggtctgag cggatttatt 2200
gacaatgaat aaagggcacg aaggccaggc cagggcctgg gcctcttgtg 2250
ctaagagggc agggggccta cggtgctatt gctttagggg cccaccacgg 2300
gcaggggcct gctcccagct gccacgtct atcatatgga gcgaggtgtt 2350
ggggaaggcg gggcaggcag cctgttgacg gcaggggaag gagaagagac 2400
tgaggggctg tgacctctcc tgaggcccc agcctgagac tgtgcaactc 2450
caggtggaag tagagctggt ccctcagctg gggggcagtg ctgtccagt 2500
gaggggaggg ctttcacgcc caccacccc ctggccctgc cagctggtag 2550
tccatcagca caatgaagga gacttgaga agaggaagaa taactgtt 2600
gcttctgtt caagctgtgt ccagcttttc ccctggggct ccaggacctt 2650
ccctacctcc accaccaaac caagggattt atagcaaagg ctaagcctgc 2700

agtttactct ggggggttcag ggagccgaaa ggcttaaata gtttaagtag 2750
 gtgatgggaa gatgagatta cctcatttag ggctcaggca gactcacctc 2800
 acatactccc tgctccctgt ggtagagaca cctgagagaa aggggagggg 2850
 tcaacaatga gagaccagga gtaggtccta tcagtgcgcc ccagagtaga 2900
 gagcaataag agcccagccc agtgcagtcc cggctgtgtt ttcctacctg 2950
 gtgatcagaa gtgtctggtt tgcttggtg cccatttgcc tcttgagtgg 3000
 gcagccctgg gcttggggcc ctccctccgg ccctcagtgt tggctctgca 3050
 gaagctctgg ggttcccttc aagtgcacga ggggttaggc tgctgtccct 3100
 gagtcccca ttctgtactg gggggctggc taggacctgg ggctgtggcc 3150
 tctcaggggg cagcctctcc atggcaggca tccctgcctt gggctgccct 3200
 cccccagacc cctgaccacc ccctgggtcc tgtccccac cagagcccca 3250
 gctcctgtct gtgggggagc catcacggtg ttcgtgcagt ccatagcgct 3300
 tctcaatgtg tgtcaccgga aacctgggag gggaggaac actggggttt 3350
 aggaccacaa ctgagaggct gcttggccct cccctctgac cagggacatc 3400
 ctgagtttgg tggctacttc cctctggcct aaggtagggg aggccttctc 3450
 agattgtggg gcacattgtg tagcctgact tctgctggag ctcccagtcc 3500
 aggaggaag agccaaggcc cacttttggg atcaggtgcc tgatcactgg 3550
 gccccctacc tcagcccccc ttccctgga gcacctgcc cacctgcca 3600
 cagagaacac agtggctctc cctgtccggg ggcggctttt tccttccttg 3650
 gagcgctcct gacggacaag tggaggcctc ttgctgcggc tgcaatggat 3700
 gcaaggggct gcagagccca ggtgcactgt gtgatgatgg gagggggctc 3750
 cgtcctgcag gctggagggt gcatccacac tggacagcag gagggggga 3800
 gtgagggtaa catttccatt tcccttcatt ttttgtttt tacgttcttt 3850
 cagcatgctc cttaaaaccc cagaagcccc aatttcccca agccccattt 3900
 tttctgtctt ttatctaata aactcaatat taag 3934

<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

Met	Gln	Leu	Ala	Lys	Tyr	Gln	Ser	His	Ser	Lys	Ser	Cys	Pro	Thr
1				5					10				15	

Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu		20	25	30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala		35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg		50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu		65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala		80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser		95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp		110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu		125	130	135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro		140	145	150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp		155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu		170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu		185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser		200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu		215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln		230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu		245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly		260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu		275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu		290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala				

305	310	315
Pro Thr Ser Val Leu Asp Gly Pro Pro	Ala Pro Val Leu Pro Gly	
320	325	330
Asp Lys Ala Leu Asp Phe Pro Gly Phe	Leu Asp Met Met Ala Pro	
335	340	345
Arg Leu Arg Pro Met Arg Pro Pro Pro	Pro Pro Pro Ala Lys Ala	
350	355	360
Pro Asp Pro Gly His Pro Asp Pro Leu Thr		
365	370	

<210> 316
 <211> 4407
 <212> DNA
 <213> Homo sapiens

<400> 316
 cacagggaga cccacagaca catatgcacg agagagacag aggaggaaag 50
 agacagagac aaaggcacag cggaagaagg cagagacagg gcaggcacag 100
 aagcggccca gacagagtcc tacagaggga gaggccagag aagctgcaga 150
 agacacaggc agggagagac aaagatccag gaaaggaggg ctcaggagga 200
 gagtttgag aagccagacc cctgggcacc tctcccaagc ccaaggacta 250
 agttttctcc atttcttta acggctctca gcccttctga aaactttgcc 300
 tctgaccttg gcaggagtcc aagccccag gctacagaga ggagctttcc 350
 aaagctaggg tgtggaggac ttggtgccct agacggcctc agtccctccc 400
 agctgcagta ccagtgccat gtcccagaca ggctcgcac ccgggagggg 450
 cttggcaggg cgctggctgt ggggagccca accctgcctc ctgctcccca 500
 ttgtgccgct ctctggctg gtgtggctgc ttctgctact gctggcctct 550
 ctctgccct cagcccggct ggccagcccc ctccccggg aggaggagat 600
 cgtgtttcca gagaagctca acggcagcgt cctgcctggc tcgggcgccc 650
 ctgccaggct gttgtgccg ttgcaggcct ttggggagac gctgtacta 700
 gagctggagc aggactccg gtgtcaggtc gaggggctga cagtgcagta 750
 cctgggccag gcgcctgagc tgctgggtgg agcagagcct ggcacctacc 800
 tgactggcac catcaatgga gatccggagt cgggtggcatc tctgcactgg 850
 gatgggggag ccctgttagg cgtgttaca tatcgggggg ctgaactcca 900
 cctccagccc ctggagggag gcaccctaa ctctgctggg ggacctgggg 950

ctacacatcct acgccggaag agtcctgccg gcggtcaagg tcccatgtgc 1000
 aacgtcaagg ctctcttgg aagccccagc cccagacccc gaagagccaa 1050
 gcgctttgct tcaactgagta gatttgtgga gacactgggtg gtggcagatg 1100
 acaagatggc cgcattccac ggtgcggggc taaagcgcta cctgctaaca 1150
 gtgatggcag cagcagccaa ggcttcaag caccgaagca tccgcaatcc 1200
 tgtcagcttg gtggtgactc ggctagtgt cctgggggtca ggcgaggagg 1250
 ggccccaaagt gggggccagt gctgcccaga ccctgcgcag cttctgtgcc 1300
 tggcagcggg gcctcaacac ccctgaggac tcggggccctg accactttga 1350
 cacagccatt ctgtttaccc gtcaggacct gtgtggagtc tccacttgcg 1400
 acacgtggg tatggctgat gtgggcaccg tctgtgaccc ggctcggagc 1450
 tgtgccattg tggaggatga tgggctccag tcagccttca ctgctgctca 1500
 tgaactgggt catgtcttca acatgctcca tgacaactcc aagccatgca 1550
 tcagtttgaa tgggcctttg agcacctctc gccatgtcat gggccctgtg 1600
 atggctcatg tggatcctga ggagccctgg tccccctgca gtgcccgtt 1650
 catcactgac ttctggaca atggctatgg gcactgtctc ttagacaaac 1700
 cagaggctcc attgcatctg cctgtgactt tccctggcaa ggactatgat 1750
 gctgaccgcc agtgccagct gaccttcggg cccgactcac gccattgtcc 1800
 acagctgccg ccgccctgtg ctgccctctg gtgctctggc cacctcaatg 1850
 gccatgccat gtgccagacc aaacactcgc cctggggccga tggcacaccc 1900
 tgcggggccc cagaggcctg catgggtggt cgctgcctcc acatggacca 1950
 gctccaggac ttcaatatc cacaggctgg tggctgggggt ccttggggac 2000
 catgggggtga ctgctctcgg acctgtgggg gtggtgtcca gttctcctcc 2050
 cgagactgca cgaggcctgt cccccgaat ggtggcaagt actgtgaggg 2100
 ccgcgtacc cgcttcgct cctgcaacac tgaggactgc ccaactggct 2150
 cagccctgac ctcccgag gagcagtgtg ctgcctacaa ccaccgacc 2200
 gacctcttca agagcttccc agggcccatg gactgggttc ctgctacac 2250
 aggcgtggcc cccagagacc agtgcaact cacctgccag gccggggcac 2300
 tgggctacta ctatgtgctg gagccacggg tggtagatgg gacccctgt 2350
 tccccggaca gctcctcgggt ctgtgtccag ggccgatgca tccatgctgg 2400

ctgtgatcgc atcattggct ccaagaagaa gtttgacaag tgcattgggt 2450
 gcggagggga cggttctggt tgcagcaagc agtcaggctc cttcaggaaa 2500
 ttcagggtacg gatacaacaa tgtgggtcact atccccgcgg gggccacca 2550
 cattcttgtc cggcagcagg gaaaccctgg ccaccggagc atctacttgg 2600
 ccctgaagct gccagatggc tcctatgccc tcaatgggtga atacacgctg 2650
 atgccctccc ccacagatgt ggtactgcct ggggcagtca gcttgcgcta 2700
 cagcggggcc actgcagcct cagagacact gtcaggccat gggccactgg 2750
 cccagccttt gacactgcaa gtcctagtgg ctggcaacct ccaggacaca 2800
 cgcctccgat acagcttctt cgtgccccgg ccgacctt caacgccacg 2850
 cccactccc caggactggc tgcaccgaag agcacagatt ctggagatcc 2900
 ttgcggcggcg cccctggcg ggcaggaaat aacctcacta tcccggctgc 2950
 cctttctggg caccggggcc tcggacttag ctgggagaaa gagagagctt 3000
 ctgttgctgc ctcatgctaa gactcagtgg ggaggggctg tgggcgtgag 3050
 acctgcccct cctctctgcc ctaatgcgca ggctggccct gccctggttt 3100
 cctgccctgg gaggcagtga tgggttagtg gatggaagg gctgacagac 3150
 agccctccat ctaaactgcc cctctgccc tgcgggtcac aggagggagg 3200
 ggaaggcag ggagggcctg ggccccagtt gtatttattt agtatttatt 3250
 cacttttatt tagcaccagg gaaggggaca aggactaggg tcctggggaa 3300
 cctgacctt gacctctcat agccctcacc ctggggctag gaaatccagg 3350
 gtggtggtga taggtataag tgggtgtgt atgctgtgt gtgtgtgtgt 3400
 gaaaatgtgt gtgtgcttat gtatgaggta caacctgttc tgctttcttc 3450
 ttctgaatt ttattttttg ggaaaagaaa agtcaagggt aggggtgggc 3500
 ttcagggagt gagggattat cttttttttt tttctttct ttctttcttt 3550
 ttttttttg agacagaatc tcgctctgtc gcccaggctg gagtgcaatg 3600
 gcacaatctc ggctcactgc atcctccgcc tcccgggttc aagtgattct 3650
 catgcctcag cctcctgagt agctgggatt acaggctcct gccaccacgc 3700
 ccagctaatt ttgttttgt ttgttttga gacagagtct cgctattgtc 3750
 accagggctg gaatgatttc agctcactgc aaccttcgcc acctgggttc 3800
 cagcaattct cctgcctcag cctcccgagt agctgagatt ataggcacct 3850

accaccacgc cgggctaatt tttgtatfff tagtagagac ggggtttcac 3900
catgttggcc aggctggctc cgaactcctg accttaggtg atccactcgc 3950
cttcatctcc caaagtgctg ggattacagg cgtgagccac cgtgcctggc 4000
cacgccaac taatffffgt atfffftagta gagacaggggt ttcacatgt 4050
tggccaggct gctcttgaac tctgacctc aggtaatcga cctgcctcgg 4100
cctcccaaag tgctgggatt acaggtgtga gccaccacgc ccggtacata 4150
ttffffaaat tgaattctac tatttatgtg atcctffffg agtcagacag 4200
atgtggttgc atcctaactc catgtctctg agcattagat ttctcatttg 4250
ccaataataa tacctccctt agaagtttgt tgtgaggatt aaataatgta 4300
aataaagaac tagcataaca ctcaaaaaaa aaaaaaaaaa aaaaaaaaaa 4350
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4400
aaggaaa 4407

<210> 317
<211> 837
<212> PRT
<213> Homo sapiens

<400> 317
Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg
1 5 10 15
Trp Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro
20 25 30
Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu
35 40 45
Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
50 55 60
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
65 70 75
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
80 85 90
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
95 100 105
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
110 115 120
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
125 130 135
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

140	145	150
Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu His Leu Gln Pro Leu 155	160	165
Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile 170	175	180
Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro Met Cys Asn 185	190	195
Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg Arg Ala 200	205	210
Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val Val 215	220	225
Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg 230	235	240
Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His 245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val 260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala 275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn 290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu 305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu 320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys 335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala 350	355	360
His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys 365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val 380	385	390
Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser 395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr 410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro 425	430	435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln	440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro	455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala	470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys	485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp	500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro	515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val	530	535	540
Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly	545	550	555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn	560	565	570
Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu	575	580	585
Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe	590	595	600
Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro	605	610	615
Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr	620	625	630
Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser	635	640	645
Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala	650	655	660
Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys	665	670	675
Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly	680	685	690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile	695	700	705
Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro	710	715	720
Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser			

	725		730		735									
Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp
				740					745					750
Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr
				755					760					765
Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro
				770					775					780
Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg
				785					790					795
Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro
				800					805					810
Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu
				815					820					825
Glu	Ile	Leu	Arg	Arg	Arg	Pro	Trp	Ala	Gly	Arg	Lys			
				830					835					

<210> 318
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 318
 ccctgaagct gccagatggc tcc 23

<210> 319
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 319
 ctgtgctctt cggtgcagcc agtc 24

<210> 320
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 320

ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 321

cagcagtggg ctctcagtc tctcaaagca aggaaagagt actgtgtgct 50
gagagacat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgtttggta tcttggccct aactctaatt gtctgtttt 200
gggggagcaa gcacttcttg ccggaggtac caaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcggaaat ggactgatg 350
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
atcttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600
gaccatgtat tggatcaatc cactctaatt atcagtttct gagttacaag 650
actttgagga ggaggagaa gatcttcact ttctgcca cgaaaaaaaa 700
gggattgaac aaaatgaaca gtgggtggtc cctcaagtga aagtagagaa 750
gaccggtcac gccagacaag caagtgagga agaacttcca ataaatgact 800
atactgaaaa tggaatagaa ttgatccca tgctggaatga gagaggttat 850
tgttgtattt actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950
tcatctgtcg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000
gggaggggtc aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050
atataataaa tgcattgctat tcaatgaatt tctgcctatg aggcattctg 1100
cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150
tggttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

<211> 317
 <212> PRT
 <213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	1	5	10	15
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	20	25	30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	35	40	45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	50	55	60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	65	70	75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	80	85	90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	95	100	105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	110	115	120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	125	130	135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	140	145	150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	155	160	165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	170	175	180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	185	190	195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	200	205	210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	215	220	225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	230	235	240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	245	250	255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	260	265	270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
 275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
 290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
 305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

gcggaactgg ctccggctgg cacctgagga gcggcgtgac cccgagggcc 50
 cagggagctg cccggctggc ctaggcaggc agccgcacca tggccagcac 100
 ggccgtgcag cttctgggct tcctgctcag cttcctgggc atggtgggca 150
 cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200
 accaacaatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250
 tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300
 tggcgtgcc ccaagacctc cagggtgcc gcgccctcat ggtcatctcc 350
 tgctgtctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400
 cacgcgctgc gccaaaggca caccgcgcaa gaccaccttt gccatcctcg 450
 gcggcaccct cttcatcctg gccggcctcc tgtgcatggt ggccgtctcc 500
 tggaccacca acgacgtggt gcagaacttc tacaaccgc tgctgcccag 550
 cggcatgaag tttgagattg gccaggccct gtacctgggc ttcattctct 600
 cgtccctctc gtcattggt ggcaccctgc tttgcctgtc ctgccaggac 650
 gaggcaccct acaggcccta ccaggccccg cccagggcca ccacgaccac 700
 tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750
 gggccccctc agtgacctcg gccacgcaca gcgggtacag gctgaacgac 800
 tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850
 gtccccggcg ggactgtcaa tggaggcagg ggttcagca caaagtttac 900
 ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaatgt 950
 ctttagagca cagggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
 atatttatgt ggggtgattg ataacaagtt taatataaag tgacttggga 1100
 gtttggtcag tggggttggt ttgtgatcca ggaataaacc ttgcggatgt 1150
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 324
 Met Ala Ser Thr Ala Val Gln Leu Leu Gly Phe Leu Leu Ser Phe
 1 5 10 15
 Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp
 20 25 30
 Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser
 35 40 45
 Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly
 50 55 60
 Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln
 65 70 75
 Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu
 80 85 90
 Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
 110 115 120
 Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala
 125 130 135
 Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro
 140 145 150
 Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr
 155 160 165
 Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu
 170 175 180
 Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln
 185 190 195
 Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala
 200 205 210
 Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val
 215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
 230 235

<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

<400> 325
 gagctcccct caggagcgcg ttagcttcac accttcggca gcaggagggc 50
 ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100
 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150
 gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200
 aaccccgta cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
 gacttcacgc catgctgcag gcagtgcgag ccctgatgat cgtaggcac 350
 gtccctgggtg ccattggcct cctggtatcc atctttgccc tgaaatgcat 400
 ccgcattggc agcatggagg actctgccaa agccaacatg aactgacct 450
 ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500
 gtgtttgcc aatgctggt gactaacttc tggatgtcca cagctaacat 550
 gtacaccggc atgggtggga tggcgcagac tgttcagacc aggtacacat 600
 ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cactactaatt 650
 ggggggtgtga tgatgtgcat cgcctgccg ggctggcac cagaagaaac 700
 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
 agcctggagg cttaaggcc agcactggct ttgggtccaa caccaaaaac 800
 aagaagatat acgatggagg tgcccgacac gaggacgagg tacaatctta 850
 tccttccaag cagcactatg tgtaatgctc taagacctct cagcacgggc 900
 ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950
 atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
 attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150
 gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200
 cccctcttc ctctagtca ataaacccat tgatgatcta tttccagct 1250

tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300
 ttctgctggt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350
 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
 cccatgatct cggtttttctt aactgtgat cttaaaagtt accaaaccaa 1450
 agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500
 tcttattaca gcaacaccat tctaggagt ttctgagctc tccactggag 1550
 tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600
 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
 taaaatgata cactatctct gtgaaatagc ctcaccacct catgtggata 1700
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
 gaggctgagg tgggaggatc acttgagccc agggaggttg gggctgcagt 2000
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100
 aggttaaaac taattcttta a 2121

<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
1				5					10					15
Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly

80										85					90				
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg					
				95					100					105					
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr					
				110					115					120					
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly					
				125					130					135					
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser					
				140					145					150					
Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val					
				155					160					165					
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val					
				170					175					180					
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala					
				185					190					195					
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser					
				200					205					210					
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe					
				215					220					225					
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile					
				230					235					240					
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro					
				245					250					255					
Ser	Lys	His	Asp	Tyr	Val														
				260															

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
 ggaaaaactg ttctcttctg tggcacagag aaccctgctt caaagcagaa 50
 gtagcagttc cggagtccag ctggctaaaa ctcaccccag aggataatgg 100
 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tggtggaatg 150
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgcggcctt 200
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggtttt catgatggcc atccttgcca 400
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600
 tggaccacgg cactggtgct gattgttggg ggagctctgt tctgctgctg 650
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700
 atcgcacaa ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc 850
 caaagaaact ttgatttact gttcttaact gcctaactct aattacagga 900
 actgtgcac agctatttat gattctataa gctatttcag cagaatgaga 950
 tattaacccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000
 taagggtggt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgtg acatttatat ctcacataga gacatgctta 1150
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgctttttcag ggaaatcatg gataggggtg aagaaggta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400
 atcctcttct ccagaggct ttttttttct tgtgtattaa attaacattt 1450
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550
 gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgagggtt catcaatata aataaaagag cagaaaaata 1700
 tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

atttttggtc tgtgaaaaat aaatttcctt cttgtacat ttctgttttag 1850
 ttttactaaa atctgtaaat actgtatitt tctgtttatt ccaaatttga 1900
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
 aatgaatgtg ttctatttgc tttatacat tatattaata aattgtacat 2000
 ttttctaatt 2010

<210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly
 1 5 10 15
 Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp
 20 25 30
 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
 35 40 45
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
 50 55 60
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
 65 70 75
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
 80 85 90
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
 110 115 120
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
 125 130 135
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
 140 145 150
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
 155 160 165
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
 170 175 180
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
 185 190 195
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
 200 205 210

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215				220						225

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329
 tcgcatggc ctctgccgga atgcagatcc tgggagtcgt cctgacactg 50
 ctgggctggg tgaatggcct ggtctcctgt gccctgccca tgtggaaggt 100
 gaccgctttc atcggcaaca gcatcgtggt ggcccagggtg gtgtgggagg 150
 gcctgtggat gtcctgcgtg gtgcagagca ccggccagat gcagtgaag 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
 cctctgtgtc atgcacctcc ttgtggccct gttcggttg ctggtctacc 300
 ttgtggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
 cgctgtgtgc tcacctgtg gattgtcttt gtcattctag gggctctgac 400
 gctaattccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
 accccttgtt ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
 ttgggctggg cggcctcagg ccttttggtg ctgggtgggg ggttgctgtg 550
 ctgcacttgc ccctcggggg ggtcccaggg cccagccat tacatggccc 600
 gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700
 gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750
 ttttgtttct gcctctgct atttttcttt tgactgagga tatttaaaat 800
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
 gctgtttctc acccttgat gatggagcca aagaggggat gctttgagat 900
 tctggatctt gacatgccca tcttagaagc cagtcaagct atggaactaa 950
 tgcggaggct gcttgctgtg ctggctttgc aacaagacag actgtcccca 1000
 agagtctctg ctgctgctgg gggctgggct tccctagatg tcaactggaca 1050
 gctgcccccc atctactca ggtctctgga gctcctctct tcaccttg 1100
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150
 cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccaggtcc 1200
 cagctatgta gacccccgc cccacctcca aactgcacc cttctgccct 1250

gccccctcg tctaccccc ttacactca catttttattc aaataaagca 1360

tgttttggtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
1				5					10					15

Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
			20						25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
			35						40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
			50						55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
			65						70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
			80						85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
			95						100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
			110						115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
			125						130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
			140						145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
			155						160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
			170						175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
			185						190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
			200						205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
			215						220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

gccaaggaga acatcatcaa agacttctct agactcaaaa ggcttccacg 50
ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100
gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150
gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtgg 200
ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250
ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300
gcaagttcta tagctccttg ttggctctcc cgcctgccct ggaaacagcc 350
cgggccctca tgtgtgtggc tgttgcctc tccttgatcg ccttgcttat 400
tggcatctgt ggcatgaagc aggtccagt cagaggtct aacgagagg 450
ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500
atcttcgttc tgattccggt gagctggaca gccaatataa tcatcagaga 550
tttctacaac ccagccatcc acataggtca gaaacgagag ctgggagcag 600
cacttttct tggctgggca agcgtgctg tcctcttcat tggaggggg 650
ctgctttgtg gattttgctg ctgcaacaga aagaagcaag ggtacagata 700
tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750
caatgcttag taagacctcc accagttatg tctaagcct ccttttggct 800
ccaagtatgg actatgggtc atgtttttta taaagtcctg ctagaaactg 850
taagtatgtg aggaggaga acttgcttta tgtctagatt tacattgata 900
cgaaagtctt aatttggtac tggtggtagg aatgaaaatg acttacttgg 950
acattctgac ttcaggtgta ttaaagcat tgactattgt tggaccaat 1000
cgctgctcca attttcatat tctaaattca agtataacca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgacct catgtattat 1100
ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150
acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1	5	10	15
Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg	20	25	30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

```

agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50
atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100
ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
agaagtatcc agtgggtggc atccccctgcc ccattcacata cctaccagtt 200
tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
tcatcatccc aggtctctgac tgagtttctt tcagttttac tgatgttctg 400
gggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

```

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

cccgcgcccg gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50

ctgctcgcgc cccgcgcgca tggctgcctc cccgcgcgcg cctgctgtcc 100

tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccagggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaata 550

agcgattctc ttcattgtatc tccaatgcc ttacactact tggtttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
gaagagttaa aacaacacat gtaaatacct tttgatattt catgggaatg 700
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336
Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
1 5 10 15
Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
20 25 30
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145 "

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

<400> 337
cggctcgagc ccgcccggaa gtgcccgagg ggccgcgatg gagctggggg 50
agccgggagc tcggtagcgc ggcgggcaag gcaggcgcca tgaccctgat 100
tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
gaccactgc ccagccgctc agggacccca acgcatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300
 cccccagcct gagacacaga ggtcaagctg cacagccaga gcccagcacg 350
 gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400
 gctacggctg aaattcctca atgattcaga gcagggtggcc agggcctggc 450
 cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
 cagcagggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
 gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
 tgtccacgag agtcggtecc ccaaattccc cctgcccgcc ggggtccgag 650
 cccggccctt cggggctgga aatcggcagc ctgctgctgc cctgctgct 700
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
 ttccctgac cgccactctg ggctggccg gcttcaccct gctcctcagt 800
 ctctggcct ttgcatgta ccgccgtag tgcctccgcg ggcgcttggc 850
 agcgctgcgc gccctccgg accttgctcc ccgcgccgcg gcgggagctg 900
 ctgcctgccc aggccgcct ctccggcctg cctcttcccg ctgccctgga 950
 gcccagccct gcgccgcaga ggactcccg gactggcgga ggccccgcc 1000
 tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050
 cgactggga gtgggtcct cggggtcggg catctgctgt cgctgcctcg 1100
 gccccgggca gagccgggcc gccccgggg cccgtcttag tgttctgcg 1150
 gaggaccag ccgcctcaa tccctgacag ctcttgggc tgagttggg 1200
 acgccaggtc ggtgggaggc tggtaaggg gagcggggag gggcagagga 1250
 gttccccga acccgtgcag attaaagtaa ctgtgaagtt ttaaaaaaa 1300
 aaaaaaaaa 1310

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Phe
1				5					10					15

Ser	Val	Leu	Ala	Cys	Leu	Leu	Val	Leu	Ala	Leu	Ala	Trp	Val	Ser
				20					25					30

Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
				35					40					45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50					55					60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125					130					135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230					235					240	
Phe	Ala	Met	Tyr	Arg	Pro										
				245											

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50

tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100

caagacccta agaaccatca gccctcagct gcacctcctc cctccaagg 150

atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttgga tgggtttgag gggttactccc tgagtgactg gctgtgcctg 300
 gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
 tggaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400
 acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
 ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
 gtccggagca cgggggatga acaactgggt agaattggagg ttgcactgtt 550
 caggccggcc actctctac tggctgacag gatgccgcct gagatgaaac 600
 aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650
 ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700
 ccttcccatt tacaactaaa actgaccaga gccccaggaa taaatggttt 750
 tcttggttc ctccttactc ccatctggac ccagtcccct gggttcctgtc 800
 tggtatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala	1	5	10	15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val	20	25	30	
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser	35	40	45	
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser	50	55	60	
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe	65	70	75	
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser	80	85	90	
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn	95	100	105	
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala	110	115	120	
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly	125	130	135	
Arg	Pro	Leu	Ser	Tyr	Trp	Leu	Thr	Gly	Cys	Arg	Leu	Arg						

<210> 341
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 341
ccctccaagg atgacaaagg cgc 23

<210> 342
<211> 29
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-29
<223> Synthetic construct.

<400> 342
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 343
atctcaggcg gcatcctgtc agcc 24

<210> 344
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 344
gtggatgcct gcaagaaggt tggg 24

<210> 345
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 345
agcttttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346
<211> 2575
<212> DNA
<213> Homo sapiens

<400> 346
tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50
actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
aaggagaaaa cgggggtaaa gggaggggaag caattcaatt tgaagtcctt 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
ggggtgaaac ttgggtcctg tggttttctg attgtaagtga agcaggtc 300
ttgcacacgc tgttggaaga tgctcaggacc aggttaagtga actggcagaa 350
aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400
gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttgga 450
gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500
ctccagttcc tctgctgct cctgatgctg ggatgcgtcc tgatgatggt 550
ggcgtggttg caccctcccc accacaccct gcaccagact gtcacagccc 600
aagccagcaa gcacagccct gaagccaggt accgcctgga ctttggggaa 650
tcccaggatt ggggtactgga agctgaggat gaggggtgaag agtacagccc 700
tctggagggc ctgccaccct ttatctcact gcgggaggat cagctgctgg 750
tgcccggtggc cttaccccag gccagaagga accagagcca gggcaggaga 800
ggtgggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850
cccaaagagg gactgggggg ctgatgagga cggggaggtg tctgaagaag 900
aggagttgac cccgttcagc ctggaccac gtggcctcca ggaggcactc 950
agtgcctgca tccccctcca gagggctctg cccgaggtgc ggcaccact 1000
gtgtctgcag cagcaccctc aggacagcct gccacagcc agcgtcatcc 1050
tctgtttcca tgatgaggcc tgggtccactc tctgctggac tgtacacagc 1100

atcctcgaca cagtgccag ggccttcctg aaggagatca tcctcgtgga 1150
 cgacctcagc cagcaaggac aactcaagtc tgctctcagc gaatatgtgg 1200
 ccaggctgga gggggtgaag ttactcagga gcaacaagag gctgggtgcc 1250
 atcagggccc ggatgctggg ggccaccaga gccaccgggg atgtgctcgt 1300
 cttcatggat gccactgcg agtgccaccc aggctggctg gagcccctcc 1350
 tcagcagaat agctggtgac aggagccgag tggatatctcc ggtgatagat 1400
 gtgattgact ggaagacttt ccagtattac cctcaaagg acctgcagcg 1450
 tggggtgttg gactggaagc tggatttcca ctgggaacct ttgccagagc 1500
 atgtgaggaa ggccctccag tccccataa gcccacatcag gagccctgtg 1550
 gtgcccggag aggtgggtggc catggacaga cattacttcc aaaacactgg 1600
 agcgtatgac tctcttatgt cgctgcgagg tggtgaaaac ctcgaactgt 1650
 ctttcaaggc ctggctctgt ggtggctctg ttgaaatcct tccctgctct 1700
 cgggtaggac acatctacca aaatcaggat tccattccc cctcagacca 1750
 ggaggccacc ctgaggaaca gggttcgcat tgctgagacc tggctgggg 1800
 cattcaaaga aaccttctac aagcatagcc cagaggcctt ctcttgagc 1850
 aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900
 ggggtgtcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950
 acccatctga acccaggccc agtttctctg gaaagctcca caacactgga 2000
 cttgggctct gtgcagactg ccaggcagaa ggggacatcc tgggctgtcc 2050
 catggtgttg gctccttgca gtgacagccg gcagcaacag tacctgcagc 2100
 acaccagcag gaaggagatt cactttggca gccacagca cctgtgcttt 2150
 gctgtcaggc aggagcagg gattcttcag aactgcacgg aggaaggcct 2200
 ggccatccac cagcagcact gggacttcca ggagaatggg atgattgtcc 2250
 acattctttc tgggaaatgc atggaagctg tggtgcaaga aaacaataaa 2300
 gatttgtacc tgcgtccgtg tgatggaaaa gcccgccagc agtggcgatt 2350
 tgaccagata aatgctgtgg atgaacgatg aatgtcaatg tcagaaggaa 2400
 aagagaattt tggccatcaa aatccagctc caagtgaacg taaagagctt 2450
 atatatttca tgaagctgat cttttgtgt gtgtgctcct tgtgttagga 2500
 gagaaaaaag ctctatgaaa gaatatagga agtttctcct tttcacacct 2550

tatttcattg actgctggct gctta 2575

<210> 347
<211> 639
<212> PRT
<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln
1				5					10					15
Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly
260	265	270
Ala Thr Arg Ala Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	
275	280	285
Cys Glu Cys His Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	
290	295	300
Ala Gly Asp Arg Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	
305	310	315
Asp Trp Lys Thr Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	
320	325	330
Gly Val Leu Asp Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	
335	340	345
Glu His Val Arg Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	
350	355	360
Ser Pro Val Val Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	
365	370	375
Phe Gln Asn Thr Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	
380	385	390
Gly Glu Asn Leu Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	
395	400	405
Ser Val Glu Ile Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	
410	415	420
Asn Gln Asp Ser His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	
425	430	435
Asn Arg Val Arg Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	
440	445	450
Thr Phe Tyr Lys His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	
455	460	465
Glu Lys Pro Asp Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	
470	475	480
Gly Cys Arg Thr Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	
485	490	495
Leu Tyr Pro Ser Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	
500	505	510
Asn Thr Gly Leu Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	
515	520	525
Ile Leu Gly Cys Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	
530	535	540
Gln Gln Gln Tyr Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe	

545	550	555
Gly Ser Pro Gln His Leu Cys Phe Ala	Val Arg Gln Glu Gln Val	
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly	Leu Ala Ile His Gln Gln	
575	580	585
His Trp Asp Phe Gln Glu Asn Gly Met	Ile Val His Ile Leu Ser	
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln	Glu Asn Asn Lys Asp Leu	
605	610	615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg Phe	
620	625	630
Asp Gln Ile Asn Ala Val Asp Glu Arg		
635		

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 348
 ggagaggtgg tggccatgga cag 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 349
 ctgtcactgc aaggagccaa cacc 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 350
 tatgtcgtg cgaggtggtg aaaacctga actgtctttc aaggc 45

<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50
ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100
tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150
tcttcatacct cccctcgaac cccaccagcc ccagcccgcc ccccggtgtgc 200
cagggggaggc ccctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcctg 300
cctggcactg cccccccagc cccccatca ggctttgagg agggggccgcc 350
ctcatcccaa tacccttggg ctatcgtgtg gggtcaccac gtgtctcgag 400
aggatggagg ggaccccaac tctgccaatc ccggatttct ggactatggt 450
tttgagccc ctcatgggct cgcaacccca caccacaact cagactccat 500
gcgaggatgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550
ggccattcct gttcgggggc cgtggggaag gtgtggaccc ccagctctat 600
gtcacaatta ccataccat catcattgtt ctctgtggcca ctggcatcat 650
cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700
agcaaggtgc cctgaggcag gaggagagcc agcagccact gacagacctg 750
tccccggctg gagtcaactgt gctggggggc ttcggggact cacctacccc 800
caccctgac catgaggagc cccgaggggg accccggcct gggatgcccc 850
acccaaggg ggctccagcc ttccagttga accggtgagg gcaggggcaa 900
tgggatggga gggcaaagag ggaaggcaac ttaggtcttc agagctgggg 950
tgggggtgcc ctctggatgg gtagtgagga ggcaggcgtg gcctcccaca 1000
gcccctggcc ctccaaggg ggctggacca gctcctctct gggaggcacc 1050
cttccttctc ccagtctctc aggatctgtg tctattctc tgctgcccac 1100
aactccaact ctgccctctt tggttttttc tcatgccacc ttgtctaaga 1150
caactctgcc ctcttaacct tgattcccc tctttgtctt gaacttcccc 1200
ttctattctg gcctaccctt tggttcctga ctgtgccctt tccctcttcc 1250
tctcaggatt cccctggtga atctgtgatg cccccaatgt tggggtgcag 1300

ccaagcagga ggccaagggg ccggcacagc ccccatccca ctgaggggtgg 1350
 ggcagctgtg gggagctggg gccacagggg ctcttggtc ctgccccttg 1400
 cacaccaccc ggaacactcc ccagccccac gggcaatcct atctgctcgc 1450
 cctcctgcag gtgggggcct cacatatctg tgacttcggg tccctgtccc 1500
 cacccttgtg cactcacatg aaagccttgc aactcacct ccaccttcac 1550
 aggccatttg cacacgctcc tgcaccctct ccccgctcat accgctccgc 1600
 tcagctgact ctcatgttct ctgctctcac atttgcactc tctccttccc 1650
 acattctgtg ctgagctcac tcagtgggtca gcgtttcctg cacactttac 1700
 ctctcatgtg cgtttcccg cctgatgttg tgggtggtgtg cggcgtgctc 1750
 actctctccc tcatgaacac ccaccacct cgtttccgca gcccctgcgt 1800
 gctgctccag aggtgggtgg gaggtgagct gggggctcct tgggccctca 1850
 tcggtcatgg tctcgtccca ttccacacca tttgtttctc tgtctccca 1900
 tctactcca aggatgccg catcacctg agggctcccc cttgggaatg 1950
 gggtagtgag gccccagact tcacccccag cccactgcta aaatctgttt 2000
 tctgacagat gggttttggg gagtcgcctg ctgcactaca tgagaaagg 2050
 actcccattt gcccttcct ttctctaca gtcccttttg tcttgtctgt 2100
 cctggctgtc tgtgtgtgtg ccattctctg gacttcagag cccctgagc 2150
 cagtctccc ttcccagcct ccctttgggc ctccctaact ccacctaggc 2200
 tgccagggac cggagtcagc tggttcaagg ccacgggag ctctgcctcc 2250
 aagtctaccc ttccctccc ggactccctc ctgtccctc ctttctccc 2300
 tcttctctc cactctcctt ccttttgctt ccctgccctt tccccctcct 2350
 caggttcttc cctccttctc actggttttt ccaccttct ccttcccttc 2400
 ttccctggct cctaggctgt gatatatatt tttgtattat ctctttcttc 2450
 ttctgtggt gatcatcttg aattactgtg ggatgtaagt ttcaaaattt 2500
 tcaaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1				5					10					15

Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	20	25	30
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	140	145	150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	155	160	165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	170	175	180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	185	190	195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	200	205	210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	215	220	225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	230	235	240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

gttaaccagc gcagtcctcc gtgcgtcccg cccgccgctg ccctcactcc 50

cggccaggat ggcacacctgt ctggccctgc gcatggcgct gctgctggct 100

tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150
 cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300
 ggaccagggc ggcgggtcgc tggggcccgg cgctatcgcg gccatcgtga 350
 tcgcccctt gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 354
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
 1 5 10 15
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
 20 25 30
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
 110 115 120

Ser

<210> 355
 <211> 2134
 <212> DNA
 <213> Homo sapiens

<400> 355
 ggccgttggc tgggtgcgcgc ctgaagggtg tggcgcgagc agcgtcgttg 50
 gttggccggc ggcgggccgc gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcaactgc cacagcaact 150
 tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200
 tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
 cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccgagg 300
 agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
 taccagggga agatgtactt ccccggtat ttccccaacg agctgcgaaa 400
 catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450
 acctggcacc aggcagctgg ggaggagggc agctctccag ggagggaccc 500
 agcctagcac ctgaaggatc aatgccatca cccgcggggg acctccccta 550
 agtagcccc agaggcgctg ggagtgttg caccgcccctc cctgaagtt 600
 tgctccatct cacgctgggg gtcaacctgg ggaccccttc cctccggggc 650
 atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700
 tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactcgc 750
 acgtcgctg ctttggctat aactgcgagt agggctcagg catcacacc 800
 acccgtgcca gggccctact gtccctgggg tcccaggctc tccttgagg 850
 gggctccccg ccttccacct ggctgtcacc gggtagggcg gggccgtggg 900
 ttcaggggcg caccacttcc aagcctgtgt cccacaggtc ctcggcgcag 950
 tggaagtcag ctgtccaggg cctcctgaac tacataaata actggcacia 1000
 gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050
 cgtgggtgag tatgtgtggg gcacaggctg gctccctcag ctcccacgtc 1100
 ctagaggggc tcccaggagg gtggaacctc aaccagctc tgcgcaggag 1150
 gcggctgcag tccttttctc cctcaaaggc ctccgaccct cagctggagg 1200
 cgggcatctt tcctaaaggg tcccataagg gtctggttcc accccatccc 1250
 aggtctgtgg tcagagcctg ggagggttcc ctacgatgt taggggtgcc 1300
 ccatggaggg gctgactgcc ccacattgcc tttcagacag gacacgagca 1350
 tgaggtaagg ccgccctgac ctggacttca gggggagggg gtaaaggag 1400
 agaggagggg ggctagggg tcctctagat cagtgggggc actgcagggtg 1450
 gggctctccc tatacctggg acacctgctg gatgtcacct ctgcaaccac 1500
 acccatgtgg tggtttcatg aacagaccac gctcctctgc cttctcctgg 1550

cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600
ggcctcggga gaaggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650
gcacaccctt cggacatccc aggcacgagg gtgtcgtgga tgtggccaca 1700
cataggacca cacgtcccag ctgggaggag aggcctgggg ccccaggga 1750
gggaggcagg ggggtggggga catggagagc tgaggcagcc tcgtctcccc 1800
gcagcctggt atcgccagcc ttaaggtgtc tggagcccc acacttgGCC 1850
aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900
gctgggcctg ccccaggga acgtgggggc ggagactcag ctggacagcc 1950
cctgcctgtc actctggagc tgggctgctg ctgcctcagg accccctctc 2000
cgacccccga cagagctgag ctggccaggg ccaggagggc gggaggagg 2050
gaatgggggt gggctgtgCG cagcatcagc gcctgggcag gtccgcagag 2100
ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala	1	5	10	15
His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser	20	25	30	
Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp	35	40	45	
Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr	50	55	60	
Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu	65	70	75	
Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln	80	85	90	
Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu	95	100	105	
Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala	110	115	120	
Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln	125	130	135	
Leu	Ser	Arg	Glu	Gly	Pro	Ser	Leu	Ala	Pro	Glu	Gly	Ser	Met	Pro				

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

agcaggagca ggagagggac aatggaagct gccccgtcca ggttcatgtt 50
cctcttattt ctctcacgt gtgagctggc tgcagaagtt gctgcagaag 100
ttgagaaatc ctcataggt cctgggtgctg cccaggaacc cacgtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250
gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300
gaggttctga cacactacaa catcactggg aacaccatct gcctctttcg 350
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
tcagattcat ctctctga taatgaacaa ggcctccca gagtatgaag 550
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
ctctttattc tgggtggacag tggtagaaa gaaaatggga aggtgatatc 650
atctttcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700
ctctagatga cgagtgggat acactgccc cagcagaagt ttccgtagag 750
catgtgcaaa acttttgtga tggattccta agtggaaaat tggtgaaaga 800
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900
aactcaaatc tcagagacac taaacaacag gatcactagg cctgccaacc 950
acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050
tctcttcttc cttcttttaa atttcatatc ctcaactcct atccaatttc 1100
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
tcaaaaacca aaggatgggt ttaaacacct ttgtgaaatt gtctttttgc 1400
cagaagttaa aggctgtctc caagtccttg aactcagcag aaatagacca 1450
tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500
caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358
<211> 273
<212> PRT
<213> Homo sapiens

<400> 358
Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu
1 5 10 15
Thr Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser
20 25 30
Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp
35 40 45
Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val
50 55 60
Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu
65 70 75
His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser
80 85 90
Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr
95 100 105
Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu
110 115 120
Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe
125 130 135
Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val
140 145 150
Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu
155 160 165
Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu Glu Asn Met His
170 175 180
Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys Ile Leu Phe
185 190 195

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 359

ccagcagtgc ccatactcca tagc 24

<210> 360

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 360

tgacgagtgg gatacactgc 20

<210> 361

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 361

gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50
ccggcgcggg tggcgagag atcagaagcc tcttcccaa gccgagcaa 100
cctcagcggg gaccgggct cagggacgcg gcggcgcgcg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggtcggg gctggcgcg gcgcttgggc 250
tcttgacagc tggagtatca gccttgaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcgggttga cctcagtcct ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
cttggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgctgtagaa aaagagaatt tgcctgtgtt 650
tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggctctca 700
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850
tgccttctgg atctcaccag ggcccagtc tataatgcaca gttagaccac 900
tccggcgga atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050
 atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100
 ggagagaaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150
 cctgatatga ggagccagtg ttgcatgatg aaaagatggt atgattctac 1200
 atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250
 caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300
 tgccttaatg gagacaatag cagatcctgt agtattttcca gtagacatgg 1350
 ccttttaatc taagggctta agactgatta gtcttagcat ttactgtagt 1400
 tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450
 cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccattgg 1500
 ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600
 tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
 attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
 cgtggagagt aaaaagtatc gggtttta 1777

<210> 364
 <211> 269
 <212> PRT
 <213> Homo sapiens

<400> 364
 Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
 1 5 10 15
 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
 20 25 30
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
 35 40 45
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
 50 55 60
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
 65 70 75
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
 80 85 90
 Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
 95 100 105

Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	110	115	120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	125	130	135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	140	145	150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	155	160	165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	170	175	180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	185	190	195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	200	205	210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	215	220	225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	230	235	240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	245	250	255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		260	265	

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

```

gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50
cgggctgccg cccccggggg cttggcctca agctgcggaac gacgcggggg 100
ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150
tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
aggggcgcgg ccccggcgca gtccccgcg gcccccgacc ctgaggcgtc 250
gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccgc 300
agaccccggc gccgccctgc tccaggtgct tcgccagagc catcgagagc 350
agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400
agtggttgga gtttctgtag atggaaaaga agtctgggtc gaaggtttag 450
gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

```

cgaattgcta gcatcagcaa aagtctcacc atgggttgctc ttgccaaatt 550
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650
 agattactga tttcccattt aagtggaatt cgtcattatg aaaaggacat 700
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850
 ttcaaaacct ggcaagaaaa agaattgattt tgaacaaggc gaattatatt 900
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
 caggaagaaa acgagccagt gatttacaat agagcaagggt aaatgaatac 1150
 cttctgctgt gtctagctat atcgcatctt aacactattt tattaattaa 1200
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300
 catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5					10					15
Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20					25					30
Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35					40					45
Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50					55					60
Arg	Gly	Ala	Ala	Pro	Ala	Gln	Ser	Pro	Ala	Ala	Pro	Asp	Pro	Glu
				65					70					75
Ala	Ser	Pro	Leu	Ala	Glu	Pro	Pro	Gln	Glu	Gln	Ser	Leu	Ala	Pro
				80					85					90

Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala	
				95					100					105	
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp	
				110					115					120	
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly	
				125					130					135	
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn	
				140					145					150	
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile	
				155					160					165	
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala	
				170					175					180	
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu	
				185					190					195	
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr	
				200					205					210	
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys	
				215					220					225	
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys	
				230					235					240	
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys	
				245					250					255	
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu	
				260					265					270	
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn	
				275					280					285	
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn	
				290					295					300	
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe	
				305					310					315	
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu	
				320					325					330	
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp	
				335					340					345	
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val	
				350					355					360	
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg			
				365					370						

<210> 367

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tgaaaagaa gtctggtcag aaggtttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggtt cattctctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacctcag aacaactcat ttgacacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
 ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150
 agtcgagccc ggggcagcgg ctgccgggccc gggactgggtg cgcgaggggc 200
 tggggcgga ggtcgagagg gcgaggcctg tggcacgggtg gggctgctgc 250
 tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300
 tcaactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
 gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
 gaagctgggtg gctatgtctc ctcccttgtc cctgcgtgct ccctggtgga 500
 gtgcacactg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
 tgggtggcggt gtcgggtggtg acgcaccccg ggggctgccg gggccatgag 600
 gtggaggacg tggacctgga gctgttcaac acctcggtgc agctgcagcc 650
 gcccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgcctgg 700
 agatggaaca ggcccagaag gccagaacc cccaggagca gaagtccttc 750
 ttcgccaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800
 gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850
 gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900
 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
 agcttcagc agccaaaagc aactgttggt ttggcaagac ggtcctgatg 1000
 tacaagcttg attgaaattc actgctcact tgatacgta ttcagaaacc 1050
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
				20					25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
				35				40						45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgtctgc tggaacccga gccggagccg gagccacagc ggggaggggtg 50

gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100

cagcaggtcg tccggggggc caccatgctg gtgactgcct accttgcttt 150

tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200

ctaaaccccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250
ctggacttct atcaggtcta cttcctggcc ctggcagctg attggcttca 300
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
cctctttctc ctgacttact cactatgctg cttaaccaaa ctctctcaag 500
actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550
ctgctcttct cagccttcga ggcttggtat atccatgagc acgtggaacg 600
gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
ctcctgtcgg accgccgct gctgctgctg ggcaccatac aagctctatt 900
tgagagtgtc atcttcatct ttgtcttctc ctggacacct gtgctggacc 950
cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100
tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150
tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200
cagcatgagc ttctacgga gaaaggtgat ccctgagaca gagcaggctg 1250
gtgtactcaa ctggttccgg gtacctctgc actcactggc ttgcctaggg 1300
ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400
tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
gaggagccct atgcccctga gctgtaacct cactccagga caagatagct 1500
gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
gggaggacat gatgggggtg atggactgga aagaaggtgc caaaagtcc 1650

ctctgtgtta ctccattta gaaaataaac actttttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
1				5					10					15

Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20					25					30

Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35					40					45

Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50					55					60

Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65					70					75

Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80					85					90

Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95					100					105

Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110					115					120

Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125					130					135

Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140					145					150

Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155					160					165

Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170					175					180

Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185					190					195

Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200					205					210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225

Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240

Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	245	250	255
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	260	265	270
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	275	280	285
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	290	295	300
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	305	310	315
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	320	325	330
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	335	340	345
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	350	355	360
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	365	370	375
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	380	385	390
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	395	400	405
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	410	415	420
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	425	430	435
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	440	445	450

<210> 375

<211> 1098

<212> DNA

<213> Artificial

<400> 375

gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50

gccctggaga tgggtccccg cgccgcgggc tgggtgttgc tcgtgctctg 100

gctccccgcg tgcgtcgcgg ccacacggctt ccgtatccat gattatttgt 150

actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200

cctgccaaagg actttggtgg tatctttcac acaaggtatg agcagattca 250

ccttgcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
 tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
 ctctccaaga ctcggtggt ccaggagcac ggcgggcggg cggatgatcat 400
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagtaccca ggcacagct gacatccccg ccctcttcct gctcggccga 500
 gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550
 catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
 aatttgagaga tagcatctgg ggacaagtgg agccaggtag aggaaaagg 750
 tttggcggtt gctaggctga aaggaagcc acaccactgg ccttccttc 800
 cccaggggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
 cccagggtt tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
 taccagggt ctctgcacag tgaccttcac agcagttgtt ggagtgggtt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5					10					15
Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
				20					25					30
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
				35					40					45
Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
				50					55					60
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
				65					70					75
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
				80					85					90

Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln
				95					100					105
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp
				110					115					120
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg
				125					130					135
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr
				140					145					150
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile
				155					160					165
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu
				170					175					180
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp							
				185										

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50
 ggctgggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctcta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
 aagacccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val	1	5	10	15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys	20	25	30	
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly	35	40	45	
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr	50	55	60	
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys	65	70	75	
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile	80	85	90	
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe	95	100	105	
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu	110	115						

<210> 379
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 379
 ctgcctccac tgctctgtgc tggg 24

<210> 380
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 380
 cagagcagtg gatgttcccc tggg 24

<210> 381
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ctttctggat gggggcccag gggggcccagg agagtataaa 50
ggcgatgtgg aggggtgcccg gcacaaccag acgcccagtc acaggcgaga 100
gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150
ctcctggggg gccccacctg ggcagggaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
ctttcctccg gggatatgtc atgtacacca gcaaggaccg ctatttctat 450
tttggaagc ttgatggcca gatctctctt gcctaccca gccaaaggagg 500
gcaggtgctg gtgggcatct atggccagta tcaactcctt ggcataaaga 550
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650
ggtatggggc catccgagct gaggccatct gtgtggtggt ggctgatggt 700
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1				5				10				15	
Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly
				20				25				30	
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile
				35				40				45	Thr

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln	50	55	60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly	65	70	75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr	80	85	90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met	95	100	105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly	110	115	120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val	125	130	135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly	140	145	150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro	155	160	165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg			170	175	

<210> 384
 <211> 2379
 <212> DNA
 <213> Homo sapiens

<400> 384
 gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50
 agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100
 atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
 cccctcccca cccccaaaa aaactgtaaa gatgcaaaa cgtaatatcc 250
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
 tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
 atgttccaaa atcgggtccat ctccaagggt gtccaatttt tcttcctggg 400
 tgtcagcgag ccctgactca ctacagtgc gctgacagg gctgtcatgc 450
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
 acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550
 cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600
 cgaggatgcc ctaagggtg taggtgtgaa ggcaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tatatctgct gggtgcttag 700
 gtttgccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
 aaagggtca accagctcac ctggctatac cttgaccata accatatacag 800
 caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
 ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900
 gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
 gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000
 ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050
 aacctggaac ttttgacct gggatataac cggatccgaa gtttagccag 1100
 gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
 atcaattttc caagctcaac ctggcccttt ttccaagggt ggtagcctt 1200
 cagaaccttt acttgacgtg gaataaaatc agtgtcatag gacagacct 1250
 gtcctggacc tggagctcct taaaaggct tgatttatca ggcaatgaga 1300
 tcgaagcttt cagtggacct agtggtttcc agtgtgtccc gaactctcag 1350
 cgcctcaacc tggattccaa caagctcaca ttattggtc aagagatttt 1400
 ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450
 aatgcagcag aaatatttgc tccctgttaa actggctgaa aagttttaaa 1500
 ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550
 agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600
 ctacagagag gtttgatctg gccagggtc tcccaaagcc gacgtttaag 1650
 cccaagctcc ccaggccgaa gcatgagagc aaacccctt tgccccgac 1700
 ggtgggagcc acagagcccg gccagagac cgatgctgac gccgagcaca 1750
 tctctttcca taaaatcatc gcgggcagcg tggcgctttt cctgtccgtg 1800
 ctctcatcc tgctggttat ctacgtgtca tggaagcgg accctgcgag 1850
 catgaagcag ctgcagcagc gctccctcat gcgaaggcac agggaaaaga 1900
 aaagacagtc cctaaagcaa atgactccca gcaccagga attttatgta 1950
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
 gggaccctgc acctataaca aatcggtc caggaggtgt gaggtatgaa 2050
 ccattgtgat aaaaagagct cttaaagct gggaaataag tgggtcttta 2100

ttgaactctg gtgactatca agggaacgcg atgccccccc tccccttccc 2150
 tctccctctc actttggtgg caagatcctt ccttggtcgt tttagtgcac 2200
 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250
 aaataccaca atcaatgtga agcttgaact ccggttttaata ataataccta 2300
 ttgtataaga ccctttactg attccattaa tgtcgcatth gttttaagat 2350
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385
 Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala
 1 5 10 15
 Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala
 20 25 30
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
 35 40 45
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
 50 55 60
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
 65 70 75
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
 80 85 90
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
 95 100 105
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
 110 115 120
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
 125 130 135
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
 140 145 150
 Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
 155 160 165
 Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
 170 175 180
 Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
 185 190 195
 Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

200					205					210				
His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe
				215					220					225
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys
				230					235					240
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu
				245					250					255
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly
				260					265					270
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu
				275					280					285
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser
				290					295					300
Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu
				305					310					315
Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe
				320					325					330
Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu
				335					340					345
Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile
				350					355					360
Cys	Gly	Lys	Ser	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ala	Arg	Ala	Leu
				365					370					375
Pro	Lys	Pro	Thr	Phe	Lys	Pro	Lys	Leu	Pro	Arg	Pro	Lys	His	Glu
				380					385					390
Ser	Lys	Pro	Pro	Leu	Pro	Pro	Thr	Val	Gly	Ala	Thr	Glu	Pro	Gly
				395					400					405
Pro	Glu	Thr	Asp	Ala	Asp	Ala	Glu	His	Ile	Ser	Phe	His	Lys	Ile
				410					415					420
Ile	Ala	Gly	Ser	Val	Ala	Leu	Phe	Leu	Ser	Val	Leu	Val	Ile	Leu
				425					430					435
Leu	Val	Ile	Tyr	Val	Ser	Trp	Lys	Arg	Tyr	Pro	Ala	Ser	Met	Lys
				440					445					450
Gln	Leu	Gln	Gln	Arg	Ser	Leu	Met	Arg	Arg	His	Arg	Lys	Lys	Lys
				455					460					465
Arg	Gln	Ser	Leu	Lys	Gln	Met	Thr	Pro	Ser	Thr	Gln	Glu	Phe	Tyr
				470					475					480
Val	Asp	Tyr	Lys	Pro	Thr	Asn	Thr	Glu	Thr	Ser	Glu	Met	Leu	Leu
				485					490					495

Asn	Gly	Thr	Gly	Pro	Cys	Thr	Tyr	Asn	Lys	Ser	Gly	Ser	Arg	Glu
				500					505					510

Cys Glu Val

<210> 386
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 386
 ctgggatctg aacagtttcg gggc 24

<210> 387
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 387
 ggtccccagg acatggtctg tccc 24

<210> 388
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

<400> 388
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
 <211> 1449
 <212> DNA
 <213> Homo sapiens

<400> 389
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
 ttgactgtcc tttaaataatg tcaagatcca gacttttcag tgtcacctca 100
 gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
 ctcgaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctgggtat atctggatcc tctgtctgct ggttttggtg 250
 gcagctcttc tctgtggagc tgtggtcctc tgccctccagt gctggctgag 300
 gagaccccgga attgattctc acaggcgcac catggcagtt tttgctggtg 350
 gagacttgga ctctatttat gggacagaag cagctgtgag tccaactgtt 400
 ggaattcacc ttcaaaactca aaccctgac ctatatcctg ttcctgctcc 450
 atgttttggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500
 caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
 tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
 ggatgttgga aaaaattttg gtcattggaga tgtttaaata gttaaagtagc 700
 aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
 attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
 gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
 tctgctttta actctttcct agcatgggtt ccataaaaaat tattataatt 900
 taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
 gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100
 tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
 ccaacacggg gagaaaagaa aatttcccct ttacagtaa tgaatgtggc 1200
 ctccatagtc catagtgttt ctctggagcc tcagggccttgc gcatattattg 1250
 cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
 agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
 ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
1				5					10				15	

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
				80					85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
				95					100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
				110					115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
				125					130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
				140					145						

<210> 391
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 391
 cttttcagtg tcacctcagc gatctc 26

<210> 392
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 392
 ccaaaacatg gagcaggaac agg 23

<210> 393
 <211> 47
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50
acccaccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcggcggcga ccgtgacgag aagccacgg ccagctcagt 200
tctcttctac tttgggagag agagaaagtc agatgccct tttaaactcc 250
ctcttcaaaa ctcatctct ggtgactga gttaatagag tggatacaac 300
cttgctgaag atgaagaata tacaatattg aggatatatt tttctttttt 350
ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
tatgtcccag aaattgagtt tactgttgct tgtatttggg ctcatttggg 500
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
gtcaagttac gtgagcaaact actagactta agcaaaagat atgttaaagc 600
tctagcagag gaaaataaga acacagtggg tgtcgagaac ggtgcttcta 650
tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700
attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttgggtgc 800
cagtaaccac aaataaaaaga acgaatgtct cgggcagtat cagatagcag 850
ttgaaaatca ctttgtgtg ctccatccac tgtggattat atcctatggc 900
agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950
aagctctaca cattttcaag gagtatgctg gattcatgga actctaattc 1000
tgtacataaa aattttaaag ttatttgttt gctttcaggc aagtctgttc 1050
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100

aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150
aatgaaaac actgaaaaac atggattcat ttctataaca cttttattta 1200
agtatataac acgttttttg gacaagtga gaatgtttaa tcattctgtc 1250
atttgttctc aatagatgta actggttagac tacggctatt tgaaaaaatg 1300
tgcttattgt actatatctt gttattccaa ttatgagcag agaaaggaaa 1350
tataatgttg aaaataatgt ttgaaatca tgacccaaag aatgtattga 1400
tttgcaactat ccttcagaat aactgaaggt taattattgt atatttttaa 1450
aaattacact tataagagta taatcttgaa atgggtagca gccactgtcc 1500
attacctatc gtaaacattg gggcaattta ataacagcat taaaatagtt 1550
gtaaactcta atcttatact tattgaagaa taaaagatat ttttatgatg 1600
agagtaacaa taaagtattc atgatttttc acatacatga atgttcattt 1650
aaaagtttaa tcctttgagt gtctatgcta tcaggaaagc acattatttc 1700
catatttggg ttaattttgc ttttattata ttgggtctagg aggaagggac 1750
tttgagagaat ggaactcttg aggactttag ccagggtgat ataataaagg 1800
tacttttgtg ctgcattaaa ttgcttgaa agtggttaaca ttatattata 1850
taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcattagat 1900
attcatttta tataatggcc acttaaaata agaacattta aaatataaac 1950
tatgaagatt gactatcttt tcaggaaaaa agctgtatat agcacaggga 2000
accctaactc tgggtaattc tagtataaaa caaattatac ttttatttaa 2050
atttcccttg tagcaaactc aattgccaca tgggtgcccta tatttcatag 2100
tatttattct ctatagtaac tgcttaagtg cagctagctt ctagatttag 2150
actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200
catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250
tttcatgaaa gacagatttc caaatctctc ttctcttctc tgtactgtct 2300
acctttatgt gaagaaatta attatatgcc attgccaggt 2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5					10					15

Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
 20 25 30
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
 35 40 45
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
 50 55 60
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
 65 70 75
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
 80 85 90
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
 95 100 105
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
 110 115 120
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
 125 130 135
 Ser Gly Ser Ile Arg
 140

<210> 396
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 396
 cgcgccggg cgcgcggggt gagcgtgccg aggcggctgt ggcgcaggct 50
 tccagccccc accatgccgt ggcccctgct gctgctgctg gccgtgagtg 100
 gggcccagac aaccgcggca tgcttccccg ggtgccaatg cgagggtggag 150
 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300
 gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350
 caccagcatc tcacccactg ctttctcccc ctttcgctac ctggagtcgc 400
 ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450
 agctcaccac tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500
 ctcaagtgtc gccttcacga cgcacagtca gggccgggca ctacacgtgg 550
 acctctccca caacctcatt caccgcctcg tgccccaccc cagaggggcc 600
 ggctgcctg cgcccacat tcagagcctg aacctggcct ggaaccggct 650

ccatgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700
 atgggaaccc tctagctgtc attggtccgg gtgccttcgc ggggctggga 750
 ggccttacac acctgtctct gccagcctg cagaggctcc ctgagctggc 800
 gccagtggc ttccgtgagc taccgggcct gcaggtcctg gacctgtcgg 850
 gcaaccccaa gcttaactgg gcaggagctg aggtgttttc aggcctgagc 900
 tccctgcagg agctggacct ttcgggcacc aacctgggtg ccctgcctga 950
 ggcgtgctc ctccacctcc cggcactgca gagcgtcagc gtgggccagg 1000
 atgtgcggtg ccggcgccctg gtgcgggagg gcacctaccc ccggaggcct 1050
 ggctccagcc ccaaggtgcc cctgcactgc gtagacaccc gggaatctgc 1100
 tgccaggggc cccaccatct tgtgacaaat ggtgtggccc agggccacat 1150
 aacagactgc tgtcctgggc tgcctcaggt cccgagtaac ttatgttcaa 1200
 tgtgccaaca ccagtgggga gccgcaggc ctatgtggca gcgtcaccac 1250
 aggagtgtg ggcctaggag aggccttggga cctgggagcc acacctagga 1300
 gcaaagtctc acccctttgt ctacgttgc tccccaaacc atgagcagag 1350
 ggacttcgat gccaaaccag actcgggtcc cctcctgctt cccttcccca 1400
 cttatccccc aagtgccttc cctcatgcct gggcggcct gaccgcgaat 1450
 gggcagaggg tgggtgggac cccctgctgc agggcagagt tcagggtccac 1500
 tgggctgagt gtcccttgg gcccatggcc cagtcactca ggggcgagtt 1550
 tcttttctaa catagccctt tctttgcat gaggccatga ggcccgttc 1600
 atccttttct atttccctag aaccttaatg gtagaaggaa ttgcaaagaa 1650
 tcaagtccac ccttctcatg tgacagatgg ggaaactgag gccttgagaa 1700
 ggaaaaaggc taatctaagt tctgcgggc agtggcatga ctggagcaca 1750
 gcctcctgcc tcccagccc gacccaatgc actttcttgt ctctctaat 1800
 aagccccacc ctcccgcct gggctcccct tgctgccctt gcctgttccc 1850
 cattagcaca ggagtagcag cagcaggaca ggcaagagcc tcacaagtgg 1900
 gactctgggc ctctgaccag ctgtgcggca tgggctaagt cactctgccc 1950
 ttgggagcct ctggaagctt agggcacatt ggttcagcc tagccagttt 2000
 ctcacctgg gttggggctc ccagcatcc agactggaaa cctaccatt 2050
 ttcccctgag catcctctag atgctgcccc aaggagttgc tgcagttctg 2100

gagcctcatc tggctgggat ctccaagggg cctcctggat tcagtcccca 2150
 ctggccctga gcacgacagc ccttcttacc ctcccaggaa tgccgtgaaa 2200
 ggagacaagg tctgcccga ccatgtctat gctctacccc cagggcagca 2250
 tctcagcttc cgaaccctgg gctgtttcct tagtcttcat tttataaaaag 2300
 ttgttgccctt ttttaacggag tgtcactttc aaccggcctc ccctaccct 2350
 gctggccggg gatggagaca tgtcatttgt aaaagcagaa aaaggttgca 2400
 tttgttact tttgtaatat tgcctgggc ctgtgttggg gtgttggggg 2450
 aagctgggca tcagtggcca catgggcatc aggggctggc cccacagaga 2500
 cccacaggg cagtgaagctc tgtcttcccc cacctgccta gcccatcatc 2550
 tatctaaccg gtccttgatt taataaacac tataaaaggt ttaaaaaaaaa 2600
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 397
 Met Pro Trp Pro Leu Leu Leu Leu Leu Ala Val Ser Gly Ala Gln
 1 5 10 15
 Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr
 20 25 30
 Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
 35 40 45
 Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
 50 55 60
 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
 65 70 75
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
 80 85 90
 Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
 95 100 105
 Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu
 110 115 120
 Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp
 125 130 135
 Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
 140 145 150

Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp Leu Ser
155	160	165
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala Gly
170	175	180
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn Arg
185	190	195
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr Leu
200	205	210
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala Phe
215	220	225
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu Gln
230	235	240
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro Gly
245	250	255
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp Ala
260	265	270
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu Asp
275	280	285
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu Leu
290	295	300
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val Arg
305	310	315
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro Gly
320	325	330
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu Ser
335	340	345
Ala Ala Arg Gly	Pro Thr Ile Leu	
350		

<210> 398

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaagggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caaccccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga aggggtgagct acgttggtt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggagggttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaaatcga 600

tgctgcctcc tgcgccattt gctaagactc tatctggaca gggatatttaa 650

aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

ccaattcctt tottaccatc aagaaggacc tccggctctc tcatgcccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800
 gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850
 gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
 acctgcagag gaggcgatgac cccaaaccac catctcttta ctgtactagt 1000
 cttgtgctgg tcacagtgtg tcttatttat gcattacttg cttccttgca 1050
 tgattgtctt tatgcatccc caatcttaat tgagaccata cttgtataag 1100
 atttttgtaa tatctttctg ctattggata tatttattag ttaatatatt 1150
 tatttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200
 ctttaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250
 gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300
 ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
 gatgctctgt gagatatatt aaattgaacc aatgactact taggatgggt 1400
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
 aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
1				5					10				15	
Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
				20					25				30	
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
				35					40				45	
Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
				50					55				60	
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
				65					70				75	
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
				80					85				90	

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

<400> 403
 ctcctgtggt ctccagattt caggccta 28

<210> 404
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccgga ggaggaggag 50
aggcttttgc cgctgacca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggtaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactcaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcgat ttacagacac gtagtgtatt ctggaggctcg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tcccctttgg aatcagtc tggagggat gatggctggg gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaattggaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650
accacttatg atacagtga acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggtg agaatgacct cttgggtcaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttta 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala			
				20					25					30			
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr			
				35					40					45			
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp			
				50					55					60			
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala			
				65					70					75			
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly			
				80					85					90			
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg			
				95					100					105			
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser			
				110					115					120			
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met			
				125					130					135			
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu			
				140					145					150			
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly			
				155					160					165			
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile			
				170					175					180			
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro			
				185					190					195			
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr			
				200					205					210			
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu			
				215					220					225			
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu			
				230					235					240			
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg			
				245					250					255			
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr			
				260					265					270			
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly			
				275					280					285			
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met			
				290					295					300			
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg			

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407
<211> 31
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-31
<223> Synthetic construct.

<400> 407
cgcgatccc gttatcgtct tgcgctactg c 31

<210> 408
<211> 34
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-34
<223> Synthetic construct.

<400> 408
gcggaattct taaaatggac tgactccact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50
tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100
cagcatttaa tgaaaaatct atgcttaaga agtaaaaatg gcaggcttcc 150
tagataatct tcgttgcca gaatgtgaat gtattgactg gagtgagaga 200
agaaatgctg tggcatctgt tgtcgcaggc atattgtttt ttacaggctg 250
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300
accatgcctt tcacacatgt ggtgtatctt ccacattggc tttcttcatg 350
ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400
ctgttttagga agaacagggt ctcgagtttg gcttttcatt ggtttcatgt 450
tgatgttttg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500
gttaccctaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600
 agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650
 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaattggag 700
 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750
 ttgaaatagt tttatgaaat ttctttattt ttcatgcat agactgttaa 800
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850
 tattcctgag atttagaact tgatctactc cctgagccag ggttacatca 900
 tcttgtcatt ttagaagtaa ccactcttgt ctctctggct gggcacggtg 950
 gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000
 ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050
 tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100
 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
 aggttgagcgt gagctgagtt tgcgccactg cactctagcc tggggggagaa 1200
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
 cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350
 ttttttggtg aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
 tttatataat gatTTTTTaa atgccc aaag gactagtttg aaagcttctt 1450
 ttaaaaagaa ttctctaat atgactttat gtgagaa 1487

<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

Met	Ala	Gly	Phe	Leu	Asp	Asn	Phe	Arg	Trp	Pro	Glu	Cys	Glu	Cys
1				5					10					15
Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20					25					30
Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala
				35					40					45
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr
				50					55					60
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val
				65					70					75

Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu
				80					85					90
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu
				95					100					105
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala
				110					115					120
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe
				125					130					135
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe
				140					145					150
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr							
				155										

<210> 411
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 411
 gtttgaggaa gctgggatac 20

<210> 412
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 412
 ccaaactcga gcacctgttc 20

<210> 413
 <211> 40
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-40
 <223> Synthetic construct.

<400> 413
 atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50
gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctggggccc 100
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcctc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtggggccc 550
tactatgtgc tttgaagacc gcatgatcat gagtcctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggttaa aagccccttt gagcagttct 900
taaagaacag ccagacaca aacaaatacg agggatggcc agagctgctg 950
gagatggagg gctgcatgcc ccgaagcca ttttaggggtg gctgtggctc 1000
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050
cccggcaggg gctgaggagg aggagcaggg ggtgctgcgt ggaaggtgct 1100
gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaacct 1150
tcccacagca catcctacct ggaagaccag cctcagaggg tccttctgga 1200
accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgccag acttgagccc aattaaattt 1300
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
 <223> Synthetic construct.

 <400> 416
 gccatagtca cgacatggat g 21

 <210> 417
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 417
 ggatggccag agctgctg 18

 <210> 418
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 418
 aaagtacaag tgtggcctca tcaagc 26

 <210> 419
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 419
 tctgactcct aagtcaggca ggag 24

 <210> 420
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 420
 attctctcca cagacagctg gttc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggccatcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gctcgtctgc tctctctctc tctctctcac tctccctcc 200
ctctctctct gcctgtccta gtcctctagt cctcaaattc ccagtcccct 250
gcacccttc ctgggacact atgttggtct ccgccctcct gctggagggtg 300
at ttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350
acatgggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtga actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600
cactggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
atgacagctt gagtgaggct gctgagagge ctcagggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900
 cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
 gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000
 ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050
 cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc 1100
 tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150
 gtgtaggaat cttgggtggc tgtctctgcc ttctcctggc tgtttatttc 1200
 attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250
 cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300
 catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350
 ggggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400
 ccttccccctg gacatctctt agagaggaat ggacccaggc tgtcattcca 1450
 ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500
 gaaatcgctg tgttggttaat gcagaganca aactctgttt agttgcaggg 1550
 gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600
 tttccctaga tatactgcgg gatctctcct taggataaag agttgctggt 1650
 gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700
 t 1701

<210> 423
 <211> 337
 <212> PRT
 <213> Homo sapiens

<400> 423
 Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
 1 5 10 15
 Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
 20 25 30
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
 35 40 45
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
 50 55 60
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
 65 70 75
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80										85					90				
Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu	Pro	Arg	Lys	Tyr	Val	Ala					
				95					100					105					
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly					
				110					115					120					
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His					
				125					130					135					
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala					
				140					145					150					
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu					
				155					160					165					
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His					
				170					175					180					
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro					
				185					190					195					
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe					
				200					205					210					
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val					
				215					220					225					
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln					
				230					235					240					
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro					
				245					250					255					
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn					
				260					265					270					
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr					
				275					280					285					
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly					
				290					295					300					
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile					
				305					310					315					
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser					
				320					325					330					
Ala	Gln	Ala	Thr	Thr	Glu	Ala													
				335															

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaaacca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgcttt gggactccct cccacaaaac tggctccgga tcaggaaca 200
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300
 ctgctgcagg aatgacacct ggtaccaga cccaccatt gaccctggga 350
 gggttgaatg tacaacagca actgcaccca catgtgttac caattttgt 400
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
 aaatcttcac gagcctcatc atccattcct tgttcccggg aggcattcctg 500
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
 agcaggagga gcagggtgaa atcctgccac ccagggaacc ccagcaggcc 600
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaata 700
 agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagtgcct 750
 cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
 tatgtgcct ggatgatatg catattaaaa catatttga aaactggaaa 1000
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

Met	Arg	Ser	Thr	Ile	Leu	Leu	Phe	Cys	Leu	Leu	Gly	Ser	Thr	Arg
1				5					10					15
Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
			20						25					30
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
			35						40					45
Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
			50						55					60
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
			65						70					75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
				80					85					90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
				95					100					105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
				110					115					120
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
				125					130					135
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp
				140					145					150
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln
				155					160					165
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp
				170					175					180
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His
				185					190					195
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln	
				200					205					

<210> 430
 <211> 1257
 <212> DNA
 <213> Homo Sapien

<400> 430
 ggagagagggc gcgcgggtga aaggcgcatt gatgcagcct gcggcggcct 50
 cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100
 ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
 gccccgccgc ctccccgcag cggctccgcg gctcctgtct gtcctgtctg 200
 ctgcagctgc ccgcgccgtc ggcgcctct gagatcccca aggggaagca 250
 aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
 aaaattgcgg agtgtacatt taaaagatg cgttcaaata gtgctctaag 550
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgtctgc 600
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700
 aattaatatt catcgcaactt cttctgtgga aggactttgt gaaggaattg 750
 gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800
 ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850
 tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900
 ttattatgcc ttggaatggt tcacttaaat gacattttta ataagtttat 950
 gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
 tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
 aagtgggttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100
 acattctctc aacctataat ttggaatatt gttgtgtct tttgtttttt 1150
 ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
 aatttgtaaa tgtaagaat tttttttata tctgttaa ataaaattatt 1250
 tccaaca 1257

<210> 431
 <211> 243
 <212> PRT
 <213> Homo Sapien

<400> 431
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
 1 5 10 15
 Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
 20 25 30
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 432
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence

<400> 432
 aggacttgcc ctcaggaa 18

<210> 433
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 433
 cgcaggacag ttgtgaaaat a 21

<210> 434
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 434
 atgacgctcg tccaaggcca c 21

<210> 435

<211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 435
 cccacctgta ccaccatgt 19

 <210> 436
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 436
 actccaggca ccatctgttc tccc 24

 <210> 437
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 437
 aagggtggc attcaagtc 19

 <210> 438
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 438
 tgacctggca aaggaagaa 19

 <210> 439
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 439
 cagccaccct ccagtccaag g 21

 <210> 440
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

 <400> 440
 gggtcgtggt ttggagaga 19

 <210> 441
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 441
 ctggccctca gagcaccaat 20

 <210> 442
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 442
 tcctccatca cttcccctag ctcca 25

 <210> 443
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 443
 ctggcaggag ttaaagttcc aaga 24

 <210> 444
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 444
 aaaggacacc gggatgtg 18

 <210> 445
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

<400> 445
 agcgtacact ctctccaggc aaccag 26

<210> 446
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 446
 caattctgga tgaggtggta ga 22

<210> 447
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 447
 caggactgag cgcttggtta 20

<210> 448
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 448
 caaagcgcca agtaccggac c 21

<210> 449
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 449
 ccagacctca gccaggaa 18

<210> 450
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 450
 ccctagtga ccccttca 18

<210> 451
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 451
 tctgacaagc agttttctga atc 23

 <210> 452
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 452
 ctctccccct cccttttctt ttgttt 26

 <210> 453
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 453
 ctctggtgcc cacagtga 18

 <210> 454
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 454
 ccatgcctgc tcagccaaga a 21

 <210> 455
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 455
 caggaaatct ggaaacctac agt 23

 <210> 456
 <211> 20
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide probe
 <400> 456
 ccttgaaaag gacccagttt 20
 <210> 457
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide probe
 <400> 457
 atgagtcgca cctgctgttc cc 22
 <210> 458
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide probe
 <400> 458
 tagcagctgc ccttggtta 18
 <210> 459
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide probe
 <400> 459
 aacagcaggt gcgactcatc ta 22
 <210> 460
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic oligonucleotide probe
 <400> 460
 tgctaggcga cgacacccag acc 23
 <210> 461
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> Synthetic oligonucleotide probe

<400> 461

tggacacgtg gcagtgga 18

<210> 462

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 462

tcatggctct gtcccatc 19

<210> 463

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 463

caccatttgt ttctctgtct ccccatc 27

<210> 464

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 464

ccggcatcct tggagtag 18

<210> 465

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 465

tccccattag cacaggagta 20

<210> 466

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 466

aggctcttgc ctgtcctgct gct 23

<210> 467

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 467

gccagagtc ccacttgt 18

<210> 468

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 468

actgctccgc ctactacga 19

<210> 469

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 469

aggcatcctc gccgtcctca 20

<210> 470

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 470

aaggccaagg tgagtccat 19

<210> 471

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 472
 tcagggtcta catcagcctc ctgc 24

 <210> 473
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 473
 aaggccaagg tgagtccat 19

 <210> 474
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 474
 cctactgagg agccctatgc 20

 <210> 475
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 475
 tccaggtgga ccccaacttca gg 22

 <210> 476
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 476
 gggaggctta taggcccaat ctgg 24

 <210> 477
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50